09/869198

1/54

FIG. 1

```
  1  AAAATGTATG GATACAACTT ACGTTTGATG AAAGATTTGG GCTTGAAGAC CCAGAAGATG
     TTTTACATAC CTATGTTGAA TGCAAACTAC TTTCTAAACC CGAACTTCTG GGTCTTCTAC

 61  ACATATGCAA GTATGATTTT GTAGAAGTTG AGGAACCCAG TGATGGAACT ATATTAGGGC
     TGTATACGTT CATACTAAAA CATCTTCAAC TCCTTGGGTC ACTACCTTGA TATAATCCCG

121  GCTGGTGTGG TTCTGGTACT GTACCAGGAA AACAGATTTC TAAAGGAAAT CAAATTAGGA
     CGACCACACC AAGACCATGA CATGGTCCTT TTGTCTAAAG ATTTCCTTTA GTTTAATCCT

 +1                       MetAsn IlePheLeu LeuAsnLeuLeu ThrGluGlu ValArgLeu
                          ]-------------------------------------------------
181  TAAGATTTGT ATCTGATGAA TATTTTCCTT CTGAACCTTC TAACAGAGGA GGTAAGATTA
     ATTCTAAACA TAGACTACTT ATAAAAGGAA GACTTGGAAG ATTGTCTCCT CCATTCTAAT

 +1  TyrSerCysThr ProArgAsn PheSerVal SerIleArgGlu GluLeuLys ArgThrAsp
     ------------------------------------------------------------------
241  TACAGCTGCA CACCTCGTAA CTTCTCAGTG TCCATAAGGG AAGAACTAAA GAGAACCGAT
     ATGTCGACGT GTGGAGCATT GAAGAGTCAC AGGTATTCCC TTCTTGATTT CTCTTGGCTA

 +1  ThrIlePheTrp ProGlyCys LeuLeuVal LysArgCysGly GlyAsnCys AlaCysCys
     ------------------------------------------------------------------
301  ACCATTTTCT GGCCAGGTTG TCTCCTGGTT AAACGCTGTG GTGGGAACTG TGCCTGTTGT
     TGGTAAAAGA CCGGTCCAAC AGAGGACCAA TTTGCGACAC CACCCTTGAC ACGGACAACA

 +1  LeuHisAsnCys AsnGluCys GlnCysVal ProSerLysVal ThrLysLys TyrHisGlu
     ------------------------------------------------------------------
361  CTCCACAATT GCAATGAATG TCAATGTGTC CCAAGCAAAG TTACTAAAAA ATACCACGAG
     GAGGTGTTAA CGTTACTTAC AGTTACACAG GGTTCGTTTC AATGATTTTT TATGGTGCTC

 +1  ValLeuGlnLeu ArgProLys ThrGlyVal ArgGlyLeuHis LysSerLeu ThrAspVal
     ------------------------------------------------------------------
421  GTCCTTCAGT TGAGACCAAA GACCGGTGTC AGGGGATTGC ACAAATCACT CACCGACGTG
     CAGGAAGTCA ACTCTGGTTT CTGGCCACAG TCCCCTAACG TGTTTAGTGA GTGGCTGCAC

 +1  AlaLeuGluHis HisGluGlu CysAspCys ValCysArgGly SerThrGly Gly
     ----------------------------------------------------------->
481  GCCCTGGAGC ACCATGAGGA GTGTGACTGT GTGTGCAGAG GGAGCACAGG AGGATAGCCG
     CGGGACCTCG TGGTACTCCT CACACTGACA CACACGTCTC CCTCGTGTCC TCCTATCGGC

541  CATCACCACC AGCAGCTCTT GCCCAGAGCT GTGCAGTGCA GTGGCTGATT CTATTAGAGA
     GTAGTGGTGG TCGTCGAGAA CGGGTCTCGA CACGTCACGT CACCGACTAA GATAATCTCT

601  ACGTATGCGT TATCTCCATC CTTAATCTCA GTTGTTTGCT TCAAGGACCT TTCATCTTCA
     TGCATACGCA ATAGAGGTAG GAATTAGAGT CAACAAACGA AGTTCCTGGA AAGTAGAAGT

661  GGATTTACAG TGCATTCTGA AAGAGGAGAC ATCAAACAGA ATTAGGAGTT GTGCAACAGC
     CCTAAATGTC ACGTAAGACT TTCTCCTCTG TAGTTTGTCT TAATCCTCAA CACGTTGTCG

721  TCTTTTGAGA GGAGGCCTAA AGGACAGGAG AAAAGGTCTT CAATCGTGGA AAGAAAATTA
     AGAAAACTCT CCTCCGGATT TCCTGTCCTC TTTTCCAGAA GTTAGCACCT TTCTTTTAAT

781  AATGTTGTAT TAAATAGATC ACCAGCTAGT TTCAGAGTTA CCATGTACGT ATTCCACTAG
     TTACAACATA ATTTATCTAG TGGTCGATCA AAGTCTCAAT GGTACATGCA TAAGGTGATC
```

FIG. 1 (CONTINUED).

841 CTGGGTTCTG TATTTCAGTT CTTTCGATAC GGCTTAGGGT AATGTCAGTA CAGGAAAAAA
GACCCAAGAC ATAAAGTCAA GAAAGCTATG CCGAATCCCA TTACAGTCAT GTCCTTTTTT

901 ACTGTGCAAG TGAGCACCTG ATTCCGTTGC CTTGCTTAAC TCTAAAGCTC CATGTCCTGG
TGACACGTTC ACTCGTGGAC TAAGGCAACG GAACGAATTG AGATTTCGAG GTACAGGACC

961 GCCTAAAATC GTATAAAATC TGGATTTTTT TTTTTTTTTT TGCTCATATT CACATATGTA
CGGATTTTAG CATATTTTAG ACCTAAAAAA AAAAAAAAAA ACGAGTATAA GTGTATACAT

1021 AACCAGAACA TTCTATGTAC TACAAACCTG GTTTTTAAAA AGGAACTATG TTGCTATGAA
TTGGTCTTGT AAGATACATG ATGTTTGGAC CAAAAATTTT TCCTTGATAC AACGATACTT

1081 TTAAACTTGT GTCGTGCTGA TAGGACAGAC TGGATTTTTC ATATTTCTTA TTAAAATTTC
AATTTGAACA CAGCACGACT ATCCTGTCTG ACCTAAAAAG TATAAAGAAT AATTTTAAAG

1141 TGCCATTTAG AAGAAGAGAA CTACATTCAT GGTTTGGAAG AGATAAACCT GAAAAGAAGA
ACGGTAAATC TTCTTCTCTT GATGTAAGTA CCAAACCTTC TCTATTTGGA CTTTTCTTCT

1201 GTGGCCTTAT CTTCACTTTA TCGATAAGTC AGTTTATTTG TTTCATTGTG TACATTTTTA
CACCGGAATA GAAGTGAAAT AGCTATTCAG TCAAATAAAC AAAGTAACAC ATGTAAAAAT

1261 TATTCTCCTT TTGACATTAT AACTGTTGGC TTTTCTAATC TTGTTAAATA TATCTATTTT
ATAAGAGGAA AACTGTAATA TTGACAACCG AAAAGATTAG AACAATTTAT ATAGATAAAA

1321 TACCAAAGGT ATTTAATATT CTTTTTTATG ACAACTTAGA TCAACTATTT TTAGCTTGGT
ATGGTTTCCA TAAATTATAA GAAAAAATAC TGTTGAATCT AGTTGATAAA AATCGAACCA

1381 AAATTTTTCT AAACACAATT GTTATAGCCA GAGGAACAAA GATGATATAA AATATTGTTG
TTTAAAAAGA TTTGTGTTAA CAATATCGGT CTCCTTGTTT CTACTATATT TTATAACAAC

1441 CTCTGACAAA AATACATGTA TTTCATTCTC GTATGGTGCT AGAGTTAGAT TAATCTGCAT
GAGACTGTTT TTATGTACAT AAAGTAAGAG CATACCACGA TCTCAATCTA ATTAGACGTA

1501 TTTAAAAAAC TGAATTGGAA TAGAATTGGT AAGTTGCAAA GACTTTTTGA AAATAATTAA
AAATTTTTTG ACTTAACCTT ATCTTAACCA TTCAACGTTT CTGAAAAACT TTTATTAATT

1561 ATTATCATAT CTTCCATTCC TGTTATTGGA GATGAAAATA AAAAGCAACT TATGAAAGTA
TAATAGTATA GAAGGTAAGG ACAATAACCT CTACTTTTAT TTTTCGTTGA ATACTTTCAT

1621 GACATTCAGA TCCAGCCATT ACTAACCTAT TCCTTTTTTG GGGAAATCTG AGCCTAGCTC
CTGTAAGTCT AGGTCGGTAA TGATTGGATA AGGAAAAAAC CCCTTTAGAC TCGGATCGAG

1681 AGAAAAACAT AAAGCACCTT GAAAAAGACT TGGCAGCTTC CTGATAAAGC GTGCTGTGCT
TCTTTTTGTA TTTCGTGGAA CTTTTTCTGA ACCGTCGAAG GACTATTTCG CACGACACGA

1741 GTGCAGTAGG AACACATCCT ATTTATTGTG ATGTTGTGGT TTTATTATCT TAAACTCTGT
CACGTCATCC TTGTGTAGGA TAAATAACAC TACAACACCA AAATAATAGA ATTTGAGACA

1801 TCCATACACT TGTATAAATA CATGGATATT TTTATGTACA GAAGTATGTC TCTTAACCAG
AGGTATGTGA ACATATTTAT GTACCTATAA AAATACATGT CTTCATACAG AGAATTGGTC

1861 TTCACTTATT GTACCTGG
AAGTGAATAA CATGGACC

FIG. 2. Predicted VEGF-like protein encoded by Incyte contig of 8/12/98

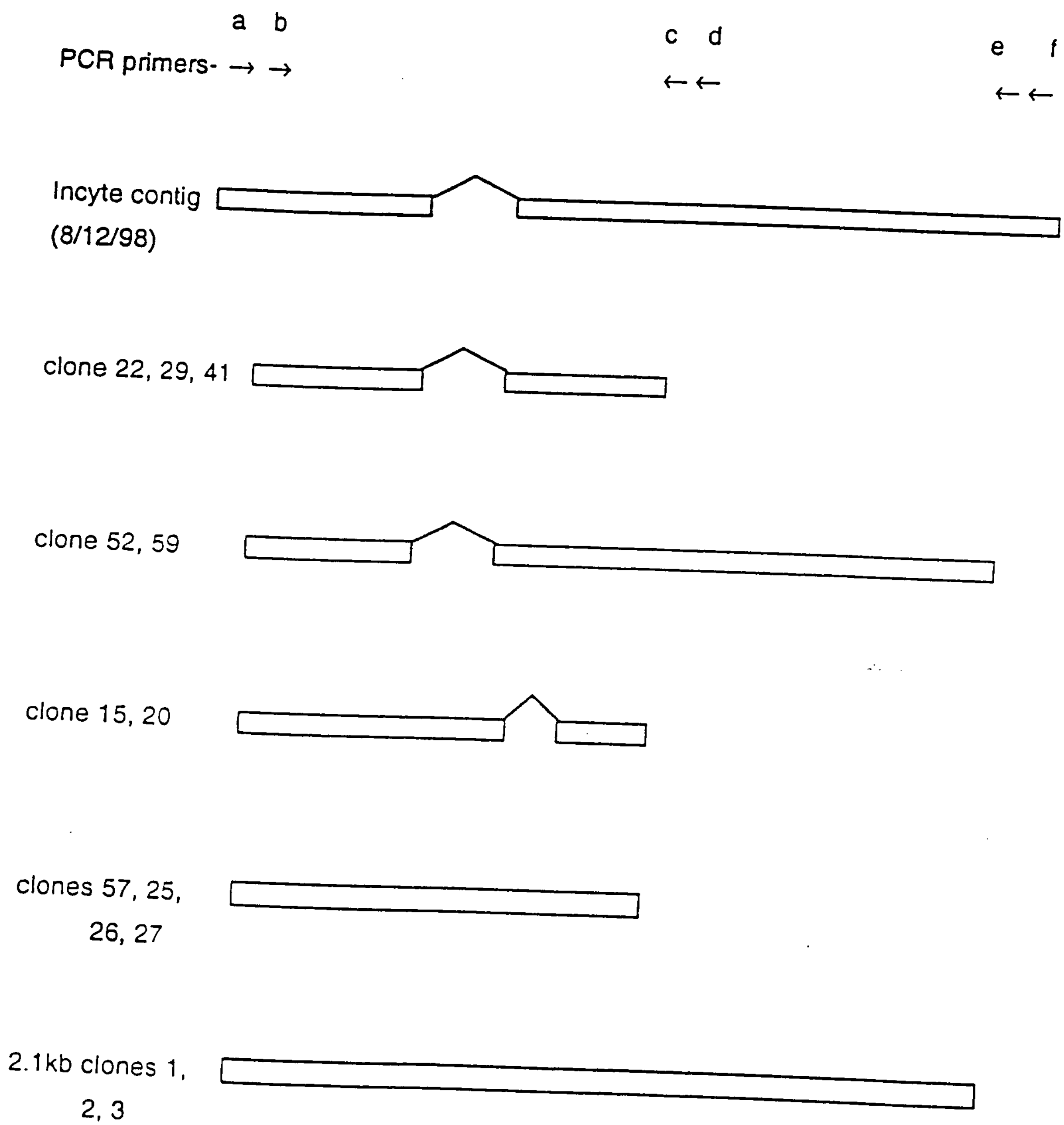
```
  1  MNIFLLNLLT EEVRLYSCTP RNFSVSIREE LKRTDTIFWP GCLLVKRCGG
 51  NCACCLHNCN ECQCVPSKVT KKYHEVLQLR PKTGVRGLHK SLTDVALEHH
101  EECDCVCRGS TGG
```

FIG. 3. PCR primers for cloning VEGF-X

vegfX1	AAAATGTATGGATACAACTTAC
vegfX2	GTTTGATGAAAGATTTGGGCTTG
vegfX3	TTTCTAAAGGAAATCAAATTAG
vegfX4	GATAAGATTTGTATCTGATG
vegfX5	GATGTCTCCTCTTTCAG
vegfX6	GCACAACTCCTAATTCTG
vegfX7	AGCACCTGATTCCGTTGC
vegfX8	TAGTACATAGAATGTTCTGG
vegfX9	AAGAGACATACTTCTGTAC
vegfX10	CCAGGTACAATAAGTGAACTG

FIG. 4.

Variants isolated by PCR (at 8/2/99, all cloned and sequenced at JRF)



primers- (see fig 3)

a- vegfX1
b- vegfX2
c- vegfX5
d- vegfX6
e- vegfX9
f- vegfX10

09/869198

FIG. 5. **VEGF-X 5' RACE primers**

vegfX11	CCTTTAGAAATCTGTTTTCCTGGTACAG
vegfX12	GGAAAATATTCATCAGATACAAATCTTATCC
vegfX13	GGTCCAGTGGCAAAGCTGAAGG
vegfX14	CTGGTTCAAGATATCGAATAAGGTCTTCC

FIG. 6. **DNA sequence assembled from in-house clones and 5'RACE**

```
  1  TGCCAGAGCA GGTGGGCGCT TCCACCCCAG TGCAGCCTTC CCCTGGCGGT GGTGAAAGAG
     ACGGTCTCGT CCACCCGCGA AGGTGGGGTC ACGTCGGAAG GGGACCGCCA CCACTTTCTC

 61  ACTCGGGAGT CGCTGCTTCC AAAGTGCCCG CCGTGAGTGA GCTCTCACCC CAGTCAGCCA
     TGAGCCCTCA GCGACGAAGG TTTCACGGGC GGCACTCACT CGAGAGTGGG GTCAGTCGGT

 +2   MetSerLeu PheGlyLeuLeu LeuLeuThr SerAlaLeu AlaGlyGlnArg GlnGlyTh
      ]-------------------------------------------------------------
121  AATGAGCCTC TTCGGGCTTC TCCTGCTGAC ATCTGCCCTG GCCGGCCAGA GACAGGGGAC
     TTACTCGGAG AAGCCCGAAG AGGACGACTG TAGACGGGAC CGGCCGGTCT CTGTCCCCTG

 +2  rGlnAlaGlu SerAsnLeuSer SerLysPhe GlnPheSer SerAsnLysGlu GlnAsnGl
     ---------------------------------------------------------------
181  TCAGGCGGAA TCCAACCTGA GTAGTAAATT CCAGTTTTCC AGCAACAAGG AACAGAACGG
     AGTCCGCCTT AGGTTGGACT CATCATTTAA GGTCAAAAGG TCGTTGTTCC TTGTCTTGCC

 +2  yValGlnAsp ProGlnHisGlu ArgIleIle ThrValSer ThrAsnGlySer IleHisSe
     ---------------------------------------------------------------
241  AGTACAAGAT CCTCAGCATG AGAGAATTAT TACTGTGTCT ACTAATGGAA GTATTCACAG
     TCATGTTCTA GGAGTCGTAC TCTCTTAATA ATGACACAGA TGATTACCTT CATAAGTGTC

 +2  rProArgPhe ProHisThrTyr ProArgAsn ThrValLeu ValTrpArgLeu ValAlaVa
     ---------------------------------------------------------------
301  CCCAAGGTTT CCTCATACTT ATCCAAGAAA TACGGTCTTG GTATGGAGAT TAGTAGCAGT
     GGGTTCCAAA GGAGTATGAA TAGGTTCTTT ATGCCAGAAC CATACCTCTA ATCATCGTCA

 +2  lGluGluAsn ValTrpIleGln LeuThrPhe AspGluArg PheGlyLeuGlu AspProGl
     ---------------------------------------------------------------
361  AGAGGAAAAT GTATGGATAC AACTTACGTT TGATGAAAGA TTTGGGCTTG AAGACCCAGA
     TCTCCTTTTA CATACCTATG TTGAATGCAA ACTACTTTCT AAACCCGAAC TTCTGGGTCT

 +2  uAspAspIle CysLysTyrAsp PheValGlu ValGluGlu ProSerAspGly ThrIleLe
     ---------------------------------------------------------------
421  AGATGACATA TGCAAGTATG ATTTTGTAGA AGTTGAGGAA CCCAGTGATG GAACTATATT
     TCTACTGTAT ACGTTCATAC TAAAACATCT TCAACTCCTT GGGTCACTAC CTTGATATAA

 +2  uGlyArgTrp CysGlySerGly ThrValPro GlyLysGln IleSerLysGly AsnGlnIl
     ---------------------------------------------------------------
481  AGGGCGCTGG TGTGGTTCTG GTACTGTACC AGGAAAACAG ATTTCTAAAG GAAATCAAAT
     TCCCGCGACC ACACCAAGAC CATGACATGG TCCTTTTGTC TAAAGATTTC CTTTAGTTTA

 +2  eArgIleArg PheValSerAsp GluTyrPhe ProSerGlu ProGlyPheCys IleHisTy
     ---------------------------------------------------------------
541  TAGGATAAGA TTTGTATCTG ATGAATATTT TCCTTCTGAA CCAGGGTTCT GCATCCACTA
     ATCCTATTCT AAACATAGAC TACTTATAAA AGGAAGACTT GGTCCCAAGA CGTAGGTGAT

 +2  rAsnIleVal MetProGlnPhe ThrGluAla ValSerPro SerValLeuPro ProSerAl
     ---------------------------------------------------------------
601  CAACATTGTC ATGCCACAAT TCACAGAAGC TGTGAGTCCT TCAGTGCTAC CCCCTTCAGC
     GTTGTAACAG TACGGTGTTA AGTGTCTTCG ACACTCAGGA AGTCACGATG GGGGAAGTCG

 +2  aLeuProLeu AspLeuLeuAsn AsnAlaIle ThrAlaPhe SerThrLeuGlu AspLeuIl
     ---------------------------------------------------------------
661  TTTGCCACTG GACCTGCTTA ATAATGCTAT AACTGCCTTT AGTACCTTGG AAGACCTTAT
     AAACGGTGAC CTGGACGAAT TATTACGATA TTGACGGAAA TCATGGAACC TTCTGGAATA
```

FIG. 6 (CONTINUED 1).

```
  +2 eArgTyrLeu GluProGluArg TrpGlnLeu AspLeuGlu AspLeuTyrArg ProThrTr
     ----------------------------------------------------------------
 721 TCGATATCTT GAACCAGAGA GATGGCAGTT GGACTTAGAA GATCTATATA GGCCAACTTG
     AGCTATAGAA CTTGGTCTCT CTACCGTCAA CCTGAATCTT CTAGATATAT CCGGTTGAAC

  +2 pGlnLeuLeu GlyLysAlaPhe ValPheGly ArgLysSer ArgValValAsp LeuAsnLe
     ----------------------------------------------------------------
 781 GCAACTTCTT GGCAAGGCTT TTGTTTTTGG AAGAAAATCC AGAGTGGTGG ATCTGAACCT
     CGTTGAAGAA CCGTTCCGAA AACAAAAACC TTCTTTTAGG TCTCACCACC TAGACTTGGA

  +2 uLeuThrGlu GluValArgLeu TyrSerCys ThrProArg AsnPheSerVal SerIleAr
     ----------------------------------------------------------------
 841 TCTAACAGAG GAGGTAAGAT TATACAGCTG CACACCTCGT AACTTCTCAG TGTCCATAAG
     AGATTGTCTC CTCCATTCTA ATATGTCGAC GTGTGGAGCA TTGAAGAGTC ACAGGTATTC

  +2 gGluGluLeu LysArgThrAsp ThrIlePhe TrpProGly CysLeuLeuVal LysArgCy
     ----------------------------------------------------------------
 901 GGAAGAACTA AAGAGAACCG ATACCATTTT CTGGCCAGGT TGTCTCCTGG TTAAACGCTG
     CCTTCTTGAT TTCTCTTGGC TATGGTAAAA GACCGGTCCA ACAGAGGACC AATTTGCGAC

  +2 sGlyGlyAsn CysAlaCysCys LeuHisAsn CysAsnGlu CysGlnCysVal ProSerLy
     ----------------------------------------------------------------
 961 TGGTGGGAAC TGTGCCTGTT GTCTCCACAA TTGCAATGAA TGTCAATGTG TCCCAAGCAA
     ACCACCCTTG ACACGGACAA CAGAGGTGTT AACGTTACTT ACAGTTACAC AGGGTTCGTT

  +2 sValThrLys LysTyrHisGlu ValLeuGln LeuArgPro LysThrGlyVal ArgGlyLe
     ----------------------------------------------------------------
1021 AGTTACTAAA AAATACCACG AGGTCCTTCA GTTGAGACCA AAGACCGGTG TCAGGGGATT
     TCAATGATTT TTTATGGTGC TCCAGGAAGT CAACTCTGGT TTCTGGCCAC AGTCCCCTAA

  +2 uHisLysSer LeuThrAspVal AlaLeuGlu HisHisGlu GluCysAspCys ValCysAr
     ----------------------------------------------------------------
1081 GCACAAATCA CTCACCGACG TGGCCCTGGA GCACCATGAG GAGTGTGACT GTGTGTGCAG
     CGTGTTTAGT GAGTGGCTGC ACCGGGACCT CGTGGTACTC CTCACACTGA CACACACGTC

  +2 gGlySerThr GlyGly
     ---------------->
1141 AGGGAGCACA GGAGGATAGC CGCATCACCA CCAGCAGCTC TTGCCCAGAG CTGTGCAGTG
     TCCCTCGTGT CCTCCTATCG GCGTAGTGGT GGTCGTCGAG AACGGGTCTC GACACGTCAC

1201 CAGTGGCTGA TTCTATTAGA GAACGTATGC GTTATCTCCA TCCTTAATCT CAGTTGTTTG
     GTCACCGACT AAGATAATCT CTTGCATACG CAATAGAGGT AGGAATTAGA GTCAACAAAC

1261 CTTCAAGGAC CTTTCATCTT CAGGATTTAC AGTGCATTCT GAAAGAGGAG ACATCAAACA
     GAAGTTCCTG GAAAGTAGAA GTCCTAAATG TCACGTAAGA CTTTCTCCTC TGTAGTTTGT

1321 GAATTAGGAG TTGTGCAACA GCTCTTTTGA GAGGAGGCCT AAAGGACAGG AGAAAAGGTC
     CTTAATCCTC AACACGTTGT CGAGAAAACT CTCCTCCGGA TTTCCTGTCC TCTTTTCCAG

1381 TTCAATCGTG GAAAGAAAAT TAAATGTTGT ATTAAATAGA TCACCAGCTA GTTTCAGAGT
     AAGTTAGCAC CTTTCTTTTA ATTTACAACA TAATTTATCT AGTGGTCGAT CAAAGTCTCA

1441 TACCATGTAC GTATTCCACT AGCTGGGTTC TGTATTTCAG TTCTTTCGAT ACGGCTTAGG
     ATGGTACATG CATAAGGTGA TCGACCCAAG ACATAAAGTC AAGAAAGCTA TGCCGAATCC

1501 GTAATGTCAG TACAGGAAAA AAACTGTGCA AGTGAGCACC TGATTCCGTT GCCTTGCTTA
     CATTACAGTC ATGTCCTTTT TTTGACACGT TCACTCGTGG ACTAAGGCAA CGGAACGAAT
```

09/869198

8/54

FIG. 6 (CONTINUED 2).

```
1561  ACTCTAAAGC TCCATGTCCT GGGCCTAAAA TCGTATAAAA TCTGGATTTT TTTTTTTTTT
      TGAGATTTCG AGGTACAGGA CCCGGATTTT AGCATATTTT AGACCTAAAA AAAAAAAAAA

1621  TTTGCTCATA TTCACATATG TAAACCAGAA CATTCTATGT ACTACAAACC TGGTTTTTAA
      AAACGAGTAT AAGTGTATAC ATTTGGTCTT GTAAGATACA TGATGTTTGG ACCAAAAATT

1681  AAAGGAACTA TGTTGCTATG AATTAAACTT GTGTCGTGCT GATAGGACAG ACTGGATTTT
      TTTCCTTGAT ACAACGATAC TTAATTTGAA CACAGCACGA CTATCCTGTC TGACCTAAAA

1741  TCATATTTCT TATTAAAATT TCTGCCATTT AGAAGAAGAG AACTACATTC ATGGTTTGGA
      AGTATAAAGA ATAATTTTAA AGACGGTAAA TCTTCTTCTC TTGATGTAAG TACCAAACCT

1801  AGAGATAAAC CTGAAAAGAA GAGTGGCCTT ATCTTCACTT TATCGATAAG CCAGTTTATT
      TCTCTATTTG GACTTTTCTT CTCACCGGAA TAGAAGTGAA ATAGCTATTC GGTCAAATAA

1861  TGTTTCATTG TGTACATTTT TATATTCTCC TTTTGACATT ATAACTGTTG GCTTTTCTAA
      ACAAAGTAAC ACATGTAAAA ATATAAGAGG AAAACTGTAA TATTGACAAC CGAAAAGATT

1921  TCTTGTTAAA TATATCTATT TTTACCAAAG GTATTTAATA TTCTTTTTTA TGACAACTTA
      AGAACAATTT ATATAGATAA AAATGGTTTC CATAAATTAT AAGAAAAAAT ACTGTTGAAT

1981  GATCAACTAT TTTTAGCTTG GTAAATTTTT CTAAACACAA TTGTTATAGC CAGAGGAACA
      CTAGTTGATA AAAATCGAAC CATTTAAAAA GATTTGTGTT AACAATATCG GTCTCCTTGT

2041  AAGATGATAT AAAATATTGT TGCTCTGACA AAAATACATG TATTTCATTC TCGTATGGTG
      TTCTACTATA TTTTATAACA ACGAGACTGT TTTTATGTAC ATAAAGTAAG AGCATACCAC

2101  CTAGAGTTAG ATTAATCTGC ATTTTAAAAA ACTGAATTGG AATAGAATTG GTAAGTTGCA
      GATCTCAATC TAATTAGACG TAAAATTTTT TGACTTAACC TTATCTTAAC CATTCAACGT

2161  AAGACTTTTT GAAAATAATT AAATTATCAT ATCTTCCATT CCTGTTATTG GAGATGAAAA
      TTCTGAAAAA CTTTTATTAA TTTAATAGTA TAGAAGGTAA GGACAATAAC CTCTACTTTT

2221  TAAAAAGCAA CTTATGAAAG TAGACATTCA GATCCAGCCA TTACTAACCT ATTCCTTTTT
      ATTTTTCGTT GAATACTTTC ATCTGTAAGT CTAGGTCGGT AATGATTGGA TAAGGAAAAA

2281  TGGGGAAATC TGAGCCTAGC TCAGAAAAAC ATAAAGCACC TTGAAAAAGA CTTGGCAGCT
      ACCCCTTTAG ACTCGGATCG AGTCTTTTTG TATTTCGTGG AACTTTTTCT GAACCGTCGA

2341  TCCTGATAAA GCGTGCTGTG CTGTGCAGTA GGAACACATC CTATTTATTG TGATGTTGTG
      AGGACTATTT CGCACGACAC GACACGTCAT CCTTGTGTAG GATAAATAAC ACTACAACAC

2401  GTTTTATTAT CTTAAACTCT GTTCCATACA CTTGTATAAA TACATGGATA TTTTTATGTA
      CAAAATAATA GAATTTGAGA CAAGGTATGT GAACATATTT ATGTACCTAT AAAAATACAT

2461  CAGAAGTATG TCTCT
      GTCTTCATAC AGAGA
```

F/G. 7. **New Sequence + Incyte ESTs**

```
  1  ATTTGTTTAA ACCTTGGGAA ACTGGTTCAG GTCCAGGTTT TGCTTTGATC CTTTTCAAAA
     TAAACAAATT TGGAACCCTT TGACCAAGTC CAGGTCCAAA ACGAAACTAG GAAAAGTTTT

 61  ACTGGAGACA CAGAAGAGGG CTTCTAGGAA AAAGTTTTGG GATGGGATTA TGTGGAAACT
     TGACCTCTGT GTCTTCTCCC GAAGATCCTT TTTCAAAACC CTACCCTAAT ACACCTTTGA

121  ACCCTGCGAT TCTCTGCTGC CAGAGCAGGC TCGGCGCTTC CACCCCAGTG CAGCCTTCCC
     TGGGACGCTA AGAGACGACG GTCTCGTCCG AGCCGCGAAG GTGGGGTCAC GTCGGAAGGG

181  CTGGCGGTGG TGAAAGAGAC TCGGGAGTCG CTGCTTCCAA AGTGCCCGCC GTGAGTGAGC
     GACCGCCACC ACTTTCTCTG AGCCCTCAGC GACGAAGGTT TCACGGGCGG CACTCACTCG

 +2                           Met SerLeuPhe GlyLeuLeu LeuLeuThrSer AlaLeuAl
                              ]-------------------------------------------
241  TCTCACCCCA GTCAGCCAAA TGAGCCTCTT CGGGCTTCTC CTGCTGACAT CTGCCCTGGC
     AGAGTGGGGT CAGTCGGTTT ACTCGGAGAA GCCCGAAGAG GACGACTGTA GACGGGACCG

 +2  aGlyGlnArg GlnGlyThrGln AlaGluSer AsnLeuSer SerLysPheGln PheSerSe
     -----------------------------------------------------------------
301  CGGCCAGAGA CAGGGGACTC AGGCGGAATC CAACCTGAGT AGTAAATTCC AGTTTTCCAG
     GCCGGTCTCT GTCCCCTGAG TCCGCCTTAG GTTGGACTCA TCATTTAAGG TCAAAAGGTC

 +2  rAsnLysGlu GlnTyrGlyVal GlnAspPro GlnHisGlu ArgIleIleThr ValSerTh
     -----------------------------------------------------------------
361  CAACAAGGAA CAGTACGGAG TACAAGATCC TCAGCATGAG AGAATTATTA CTGTGTCTAC
     GTTGTTCCTT GTCATGCCTC ATGTTCTAGG AGTCGTACTC TCTTAATAAT GACACAGATG

 +2  rAsnGlySer IleHisSerPro ArgPhePro HisThrTyr ProArgAsnThr ValLeuVa
     -----------------------------------------------------------------
421  TAATGGAAGT ATTCACAGCC CAAGGTTTCC TCATACTTAT CCAAGAAATA CGGTCTTGGT
     ATTACCTTCA TAAGTGTCGG GTTCCAAAGG AGTATGAATA GGTTCTTTAT GCCAGAACCA

 +2  lTrpArgLeu ValAlaValGlu GluAsnVal TrpIleGln LeuThrPheAsp GluArgPh
     -----------------------------------------------------------------
481  ATGGAGATTA GTAGCAGTAG AGGAAAATGT ATGGATACAA CTTACGTTTG ATGAAAGATT
     TACCTCTAAT CATCGTCATC TCCTTTTACA TACCTATGTT GAATGCAAAC TACTTTCTAA

 +2  eGlyLeuGlu AspProGluAsp AspIleCys LysTyrAsp PheValGluVal GluGluPr
     -----------------------------------------------------------------
541  TGGGCTTGAA GACCCAGAAG ATGACATATG CAAGTATGAT TTTGTAGAAG TTGAGGAACC
     ACCCGAACTT CTGGGTCTTC TACTGTATAC GTTCATACTA AAACATCTTC AACTCCTTGG

 +2  oSerAspGly ThrIleLeuGly ArgTrpCys GlySerGly ThrValProGly LysGlnIl
     -----------------------------------------------------------------
601  CAGTGATGGA ACTATATTAG GGCGCTGGTG TGGTTCTGGT ACTGTACCAG GAAAACAGAT
     GTCACTACCT TGATATAATC CCGCGACCAC ACCAAGACCA TGACATGGTC CTTTTGTCTA

 +2  eSerLysGly AsnGlnIleArg IleArgPhe ValSerAsp GluTyrPhePro SerGluPr
     -----------------------------------------------------------------
661  TTCTAAAGGA AATCAAATTA GGATAAGATT TGTATCTGAT GAATATTTTC CTTCTGAACC
     AAGATTTCCT TTAGTTTAAT CCTATTCTAA ACATAGACTA CTTATAAAAG GAAGACTTGG
```

FIG. 7(CONTINUED 1).

```
  +2 oGlyPheCys IleHisTyrAsn IleValMet ProGlnPhe ThrGluAlaVal SerProSe
     ------------------------------------------------------------------
 721 AGGGTTCTGC ATCCACTACA ACATTGTCAT GCCACAATTC ACAGAAGCTG TGAGTCCTTC
     TCCCAAGACG TAGGTGATGT TGTAACAGTA CGGTGTTAAG TGTCTTCGAC ACTCAGGAAG

  +2 rValLeuPro ProSerAlaLeu ProLeuAsp LeuLeuAsn AsnAlaIleThr AlaPheSe
     ------------------------------------------------------------------
 781 AGTGCTACCC CCTTCAGCTT TGCCACTGGA CCTGCTTAAT AATGCTATAA CTGCCTTTAG
     TCACGATGGG GGAAGTCGAA ACGGTGACCT GGACGAATTA TTACGATATT GACGGAAATC

  +2 rThrLeuGlu AspLeuIleArg TyrLeuGlu ProGluArg TrpGlnLeuAsp LeuGluAs
     ------------------------------------------------------------------
 841 TACCTTGGAA GACCTTATTC GATATCTTGA ACCAGAGAGA TGGCAGTTGG ACTTAGAAGA
     ATGGAACCTT CTGGAATAAG CTATAGAACT TGGTCTCTCT ACCGTCAACC TGAATCTTCT

  +2 pLeuTyrArg ProThrTrpGln LeuLeuGly LysAlaPhe ValPheGlyArg LysSerAr
     ------------------------------------------------------------------
 901 TCTATATAGG CCAACTTGGC AACTTCTTGG CAAGGCTTTT GTTTTTGGAA GAAAATCCAG
     AGATATATCC GGTTGAACCG TTGAAGAACC GTTCCGAAAA CAAAAACCTT CTTTTAGGTC

  +2 gValValAsp LeuAsnLeuLeu ThrGluGlu ValArgLeu TyrSerCysThr ProArgAs
     ------------------------------------------------------------------
 961 AGTGGTGGAT CTGAACCTTC TAACAGAGGA GGTAAGATTA TACAGCTGCA CACCTCGTAA
     TCACCACCTA GACTTGGAAG ATTGTCTCCT CCATTCTAAT ATGTCGACGT GTGGAGCATT

  +2 nPheSerVal SerIleArgGlu GluLeuLys ArgThrAsp ThrIlePheTrp ProGlyCy
     ------------------------------------------------------------------
1021 CTTCTCAGTG TCCATAAGGG AAGAACTAAA GAGAACCGAT ACCATTTTCT GGCCAGGTTG
     GAAGAGTCAC AGGTATTCCC TTCTTGATTT CTCTTGGCTA TGGTAAAAGA CCGGTCCAAC

  +2 sLeuLeuVal LysArgCysGly GlyAsnCys AlaCysCys LeuHisAsnCys AsnGluCy
     ------------------------------------------------------------------
1081 TCTCCTGGTT AAACGCTGTG GTGGGAACTG TGCCTGTTGT CTCCACAATT GCAATGAATG
     AGAGGACCAA TTTGCGACAC CACCCTTGAC ACGGACAACA GAGGTGTTAA CGTTACTTAC

  +2 sGlnCysVal ProSerLysVal ThrLysLys TyrHisGlu ValLeuGlnLeu ArgProLy
     ------------------------------------------------------------------
1141 TCAATGTGTC CCAAGCAAAG TTACTAAAAA ATACCACGAG GTCCTTCAGT TGAGACCAAA
     AGTTACACAG GGTTCGTTTC AATGATTTTT TATGGTGCTC CAGGAAGTCA ACTCTGGTTT

  +2 sThrGlyVal ArgGlyLeuHis LysSerLeu ThrAspVal AlaLeuGluHis HisGluGl
     ------------------------------------------------------------------
1201 GACCGGTGTC AGGGGATTGC ACAAATCACT CACCGACGTG GCCCTGGAGC ACCATGAGGA
     CTGGCCACAG TCCCCTAACG TGTTTAGTGA GTGGCTGCAC CGGGACCTCG TGGTACTCCT

  +2 uCysAspCys ValCysArgGly SerThrGly Gly
     ----------------------------------->
1261 GTGTGACTGT GTGTGCAGAG GGAGCACAGG AGGATAGCCG CATCACCACC AGCAGCTCTT
     CACACTGACA CACACGTCTC CCTCGTGTCC TCCTATCGGC GTAGTGGTGG TCGTCGAGAA

1321 GCCCAGAGCT GTGCAGTGCA GTGGCTGATT CTATTAGAGA ACGTATGCGT TATCTCCATC
     CGGGTCTCGA CACGTCACGT CACCGACTAA GATAATCTCT TGCATACGCA ATAGAGGTAG

1381 CTTAATCTCA GTTGTTTGCT TCAAGGACCT TTCATCTTCA GGATTTACAG TGCATTCTGA
     GAATTAGAGT CAACAAACGA AGTTCCTGGA AAGTAGAAGT CCTAAATGTC ACGTAAGACT
```

FIG. 7 (CONTINUED 2)

```
1441  AAGAGGAGAC ATCAAACAGA ATTAGGAGTT GTGCAACAGC TCTTTTGAGA GGAGGCCTAA
      TTCTCCTCTG TAGTTTGTCT TAATCCTCAA CACGTTGTCG AGAAAACTCT CCTCCGGATT

1501  AGGACAGGAG AAAAGGTCTT CAATCGTGGA AAGAAAATTA AATGTTGTAT TAAATAGATC
      TCCTGTCCTC TTTTCCAGAA GTTAGCACCT TTCTTTTAAT TTACAACATA ATTTATCTAG

1561  ACCAGCTAGT TTCAGAGTTA CCATGTACGT ATTCCACTAG CTGGGTTCTG TATTTCAGTT
      TGGTCGATCA AAGTCTCAAT GGTACATGCA TAAGGTGATC GACCCAAGAC ATAAAGTCAA

1621  CTTTCGATAC GGCTTAGGGT AATGTCAGTA CAGGAAAAAA ACTGTGCAAG TGAGCACCTG
      GAAAGCTATG CCGAATCCCA TTACAGTCAT GTCCTTTTTT TGACACGTTC ACTCGTGGAC

1681  ATTCCGTTGC CTTGGCTTAA CTCTAAAGCT CCATGTCCTG GGCCTAAAAT CGTATAAAAT
      TAAGGCAACG GAACCGAATT GAGATTTCGA GGTACAGGAC CCGGATTTTA GCATATTTTA

1741  CTGGATTTTT TTTTTTTTTT TTGCGCATAT TCACATATGT AAACCAGAAC ATTCTATGTA
      GACCTAAAAA AAAAAAAAAA AACGCGTATA AGTGTATACA TTTGGTCTTG TAAGATACAT

1801  CTACAAACCT GGTTTTTAAA AAGGAACTAT GTTGCTATGA ATTAAACTTG TGTCATGCTG
      GATGTTTGGA CCAAAAATTT TTCCTTGATA CAACGATACT TAATTTGAAC ACAGTACGAC

1861  ATAGGACAGA CTGGATTTTT CATATTTCTT ATTAAAATTT CTGCCATTTA GAAGAAGAGA
      TATCCTGTCT GACCTAAAAA GTATAAAGAA TAATTTTAAA GACGGTAAAT CTTCTTCTCT

1921  ACTACATTCA TGGTTTGGAA GAGATAAACC TGAAAAGAAG AGTGGCCTTA TCTTCACTTT
      TGATGTAAGT ACCAAACCTT CTCTATTTGG ACTTTTCTTC TCACCGGAAT AGAAGTGAAA

1981  ATCGATAAGT CAGTTTATTT GTTTCATTGT GTACATTTTT ATATTCTCCT TTTGACATTA
      TAGCTATTCA GTCAAATAAA CAAAGTAACA CATGTAAAAA TATAAGAGGA AAACTGTAAT

2041  TAACTGTTGG CTTTTCTAAT CTTGTTAAAT ATATCTATTT TTACCAAAGG TATTTAATAT
      ATTGACAACC GAAAAGATTA GAACAATTTA TATAGATAAA AATGGTTTCC ATAAATTATA

2101  TCTTTTTTAT GACAACTTAG ATCAACTATT TTTAGCTTGG TAAATTTTTC TAAACACAAT
      AGAAAAAATA CTGTTGAATC TAGTTGATAA AAATCGAACC ATTTAAAAAG ATTTGTGTTA

2161  TGTTATAGCC AGAGGAACAA AGATGATATA AAATATTGTT GCTCTGACAA AAATACATGT
      ACAATATCGG TCTCCTTGTT TCTACTATAT TTTATAACAA CGAGACTGTT TTTATGTACA

2221  ATTTCATTCT CGTATGGTGC TAGAGTTAGA TTAATCTGCA TTTTAAAAAA CTGAATTGGA
      TAAAGTAAGA GCATACCACG ATCTCAATCT AATTAGACGT AAAATTTTTT GACTTAACCT

2281  ATAGAATTGG TAAGTTGCAA AGACTTTTTG AAAATAATTA AATTATCATA TCTTCCATTC
      TATCTTAACC ATTCAACGTT TCTGAAAAAC TTTTATTAAT TTAATAGTAT AGAAGGTAAG

2341  CTGTTATTGG AGATGAAAAT AAAAAGCAAC TTATGAAAGT AGACATTCAG ATCCAGCCAT
      GACAATAACC TCTACTTTTA TTTTTCGTTG AATACTTTCA TCTGTAAGTC TAGGTCGGTA

2401  TACTAACCTA TTCCTTTTTT GGGGAAATCT GAGCCTAGCT CAGAAAAACA TAAAGCACCT
      ATGATTGGAT AAGGAAAAAA CCCCTTTAGA CTCGGATCGA GTCTTTTTGT ATTTCGTGGA

2461  TGAAAAAGAC TTGGCAGCTT CCTGATAAAG CGTGCTGTGC TGTGCAGTAG GAACACATCC
      ACTTTTTCTG AACCGTCGAA GGACTATTTC GCACGACACG ACACGTCATC CTTGTGTAGG

2521  TATTTATTGT GATGTTGTGG TTTTATTATC TTAAACTCTG TTCCATACAC TTGTATAAAT
      ATAAATAACA CTACAACACC AAAATAATAG AATTTGAGAC AAGGTATGTG AACATATTTA
```

FIG. 7 (CONTINUED 3).

```
2581  ACATGGATAT TTTTATGTAC AGAAGTATGT CTCTTAACCA GTTCACTTAT TGTACTCTGG
      TGTACCTATA AAAATACATG TCTTCATACA GAGAATTGGT CAAGTGAATA ACATGAGACC

2641  CAATTTAAAA GAAAATCAGT AAAATATTTT GCTTGTAAAA TGCTTAATAT CGTGCCTAGG
      GTTAAATTTT CTTTTAGTCA TTTTATAAAA CGAACATTTT ACGAATTATA GCACGGATCC

2701  TTATGTGGTG ACTATTTGAA TCAAAAATGT ATTGAATCAT CAAATAAAAG AATGTGGCTA
      AATACACCAC TGATAAACTT AGTTTTTACA TAACTTAGTA GTTTATTTTC TTACACCGAT

2761  TTTTGGGGAG AAAATT
      AAAACCCCTC TTTTAA
```

FIG. 8. **Additional oligonucleotides used for amplification of entire coding region**

5'-1	TTTGTTTAAACCTTGGGAAACTGG
5'-2	GTCCAGGTTTTGCTTTGATCC

09/869198

13/54

FIG. 9. **DNA Sequence Of Clones 4 & 7, Identical Clones Containing The Entire Open Reading Frame**

```
  1  TTTGTTTAAA CCTTGGGAAA CTGGTTCAGG TCCAGGTTTT GCTTTGATCC TTTTCAAAAA
     AAACAAATTT GGAACCCTTT GACCAAGTCC AGGTCCAAAA CGAAACTAGG AAAAGTTTTT

 61  CTGGAGACAC AGAAGAGGGC TCTAGGAAAA AGTTTTGGAT GGGATTATGT GGAAACTACC
     GACCTCTGTG TCTTCTCCCG AGATCCTTTT TCAAAACCTA CCCTAATACA CCTTTGATGG

121  CTGCGATTCT CTGCTGCCAG AGCAGGCTCG GCGCTTCCAC CCCAGTGCAG CCTTCCCCTG
     GACGCTAAGA GACGACGGTC TCGTCCGAGC CGCGAAGGTG GGGTCACGTC GGAAGGGGAC

181  GCGGTGGTGA AAGAGACTCG GGAGTCGCTG CTTCCAAAGT GCCCGCCGTG AGTGAGCTCT
     CGCCACCACT TTCTCTGAGC CCTCAGCGAC GAAGGTTTCA CGGGCGGCAC TCACTCGAGA

 +2                          MetSer LeuPheGly LeuLeuLeu LeuThrSerAla LeuAlaGl
                             ]-------------------------------------------------
241  CACCCCAGTC AGCCAAATGA GCCTCTTCGG GCTTCTCCTG CTGACATCTG CCCTGGCCGG
     GTGGGGTCAG TCGGTTTACT CGGAGAAGCC CGAAGAGGAC GACTGTAGAC GGGACCGGCC

 +2  yGlnArgGln GlyThrGlnAla GluSerAsn LeuSerSer LysPheGlnPhe SerSerAs
     -------------------------------------------------------------------
301  CCAGAGACAG GGGACTCAGG CGGAATCCAA CCTGAGTAGT AAATTCCAGT TTCCAGCAA
     GGTCTCTGTC CCCTGAGTCC GCCTTAGGTT GGACTCATCA TTTAAGGTCA AAAGGTCGTT

 +2  nLysGluGln AsnGlyValGln AspProGln HisGluArg IleIleThrVal SerThrAs
     -------------------------------------------------------------------
361  CAAGGAACAG AACGGAGTAC AAGATCCTCA GCATGAGAGA ATTATTACTG TGTCTACTAA
     GTTCCTTGTC TTGCCTCATG TTCTAGGAGT CGTACTCTCT TAATAATGAC ACAGATGATT

 +2  nGlySerIle HisSerProArg PheProHis ThrTyrPro ArgAsnThrVal LeuValTr
     -------------------------------------------------------------------
421  TGGAAGTATT CACAGCCCAA GGTTTCCTCA TACTTATCCA AGAAATACGG TCTTGGTATG
     ACCTTCATAA GTGTCGGGTT CCAAAGGAGT ATGAATAGGT TCTTTATGCC AGAACCATAC

 +2  pArgLeuVal AlaValGluGlu AsnValTrp IleGlnLeu ThrPheAspGlu ArgPheGl
     -------------------------------------------------------------------
481  GAGATTAGTA GCAGTAGAGG AAAATGTATG GATACAACTT ACGTTTGATG AAAGATTTGG
     CTCTAATCAT CGTCATCTCC TTTTACATAC CTATGTTGAA TGCAAACTAC TTTCTAAACC

 +2  yLeuGluAsp ProGluAspAsp IleCysLys TyrAspPhe ValGluValGlu GluProSe
     -------------------------------------------------------------------
541  GCTTGAAGAC CCAGAAGATG ACATATGCAA GTATGATTTT GTAGAAGTTG AGGAACCCAG
     CGAACTTCTG GGTCTTCTAC TGTATACGTT CATACTAAAA CATCTTCAAC TCCTTGGGTC

 +2  rAspGlyThr IleLeuGlyArg TrpCysGly SerGlyThr ValProGlyLys GlnIleSe
     -------------------------------------------------------------------
601  TGATGGAACT ATATTAGGGC GCTGGTGTGG TTCTGGTACT GTACCAGGAA AACAGATTTC
     ACTACCTTGA TATAATCCCG CGACCACACC AAGACCATGA CATGGTCCTT TTGTCTAAAG

 +2  rLysGlyAsn GlnIleArgIle ArgPheVal SerAspGlu TyrPheProSer GluProGl
     -------------------------------------------------------------------
661  TAAAGGAAAT CAAATTAGGA TAAGATTTGT ATCTGATGAA TATTTTCCTT CTGAACCAGG
     ATTTCCTTTA GTTTAATCCT ATTCTAAACA TAGACTACTT ATAAAAGGAA GACTTGGTCC
```

FIG. 9 (CONTINUED). 14/54

```
  +2 yPheCysIle HisTyrAsnIle ValMetPro GlnPheThr GluAlaValSer ProSerVa
     ------------------------------------------------------------------
 721 GTTCTGCATC CACTACAACA TTGTCATGCC ACAATTCACA GAAGCTGTGA GTCCTTCAGT
     CAAGACGTAG GTGATGTTGT AACAGTACGG TGTTAAGTGT CTTCGACACT CAGGAAGTCA

  +2 lLeuProPro SerAlaLeuPro LeuAspLeu LeuAsnAsn AlaIleThrAla PheSerTh
     ------------------------------------------------------------------
 781 GCTACCCCCT TCAGCTTTGC CACTGGACCT GCTTAATAAT GCTATAACTG CCTTTAGTAC
     CGATGGGGGA AGTCGAAACG GTGACCTGGA CGAATTATTA CGATATTGAC GGAAATCATG

  +2 rLeuGluAsp LeuIleArgTyr LeuGluPro GluArgTrp GlnLeuAspLeu GluAspLe
     ------------------------------------------------------------------
 841 CTTGGAAGAC CTTATTCGAT ATCTTGAACC AGAGAGATGG CAGTTGGACT TAGAAGATCT
     GAACCTTCTG GAATAAGCTA TAGAACTTGG TCTCTCTACC GTCAACCTGA ATCTTCTAGA

  +2 uTyrArgPro ThrTrpGlnLeu LeuGlyLys AlaPheVal PheGlyArgLys SerArgVa
     ------------------------------------------------------------------
 901 ATATAGGCCA ACTTGGCAAC TTCTTGGCAA GGCTTTTGTT TTTGGAAGAA AATCCAGAGT
     TATATCCGGT TGAACCGTTG AAGAACCGTT CCGAAAACAA AAACCTTCTT TTAGGTCTCA

  +2 lValAspLeu AsnLeuLeuThr GluGluVal ArgLeuTyr SerCysThrPro ArgAsnPh
     ------------------------------------------------------------------
 961 GGTGGATCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC AGCTGCACAC CTCGTAACTT
     CCACCTAGAC TTGGAAGATT GTCTCCTCCA TTCTAATATG TCGACGTGTG GAGCATTGAA

  +2 eSerValSer IleArgGluGlu LeuLysArg ThrAspThr IlePheTrpPro GlyCysLe
     ------------------------------------------------------------------
1021 CTCAGTGTCC ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTTCTGGC CAGGTTGTCT
     GAGTCACAGG TATTCCCTTC TTGATTTCTC TTGGCTATGG TAAAAGACCG GTCCAACAGA

  +2 uLeuValLys ArgCysGlyGly AsnCysAla CysCysLeu HisAsnCysAsn GluCysGl
     ------------------------------------------------------------------
1081 CCTGGTTAAA CGCTGTGGTG GAACTGTGCC TGTTGTCTC CACAATTGCA ATGAATGTCA
     GGACCAATTT GCGACACCAC CCTTGACACG GACAACAGAG GTGTTAACGT TACTTACAGT

  +2 nCysValPro SerLysValThr LysLysTyr HisGluVal LeuGlnLeuArg ProLysTh
     ------------------------------------------------------------------
1141 ATGTGTCCCA AGCAAAGTTA CTAAAAAATA CCACGAGGTC CTTCAGTTGA GACCAAAGAC
     TACACAGGGT TCGTTTCAAT GATTTTTTAT GGTGCTCCAG GAAGTCAACT CTGGTTTCTG

  +2 rGlyValArg GlyLeuHisLys SerLeuThr AspValAla LeuGluHisHis GluGluCy
     ------------------------------------------------------------------
1201 CGGTGTCAGG GGATTGCACA AATCACTCAC CGACGTGGCC CTGGAGCACC ATGAGGAGTG
     GCCACAGTCC CCTAACGTGT TTAGTGAGTG GCTGCACCGG GACCTCGTGG TACTCCTCAC

  +2 sAspCysVal CysArgGlySer ThrGlyGly
     --------------------------------->
1261 TGACTGTGTG TGCAGAGGGA GCACAGGAGG ATAGCCGCAT CACCACCAGC AGCTCTTGCC
     ACTGACACAC ACGTCTCCCT CGTGTCCTCC TATCGGCGTA GTGGTGGTCG TCGAGAACGG

1321 CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAACG TATGCGTTAT CTCCATCCTT
     GTCTCGACAC GTCACGTCAC CGACTAAGAT AATCTCTTGC ATACGCAATA GAGGTAGGAA

1381 AATCTCAGTT GTTTGCTTCA AGGACCTTTC ATCTTCAGGA TTTACAGTGC ATTCTGAAAG
     TTAGAGTCAA CAAACGAAGT TCCTGGAAAG TAGAAGTCCT AAATGTCACG TAAGACTTTC

1441 AGGAGACATC AAACAGAATT AGGAGTTGTG CAA
     TCCTCTGTAG TTTGTCTTAA TCCTCAACAC GTT
```

FIG. 10. **Predicted Full-length Polypeptide Sequence**

1 MSLFGLLLLT SALAGQRQGT QAESNLSSKF QFSSNKEQYG VQDPQHERII

51 TVSTNGSIHS PRFPHTYPRN TVLVWRLVAV EENVWIQLTF DERFGLEDPE

101 DDICKYDFVE VEEPSDGTIL GRWCGSGTVP GKQISKGNQI RIRFVSDEYF

151 PSEPGFCIHY NIVMPQFTEA VSPSVLPPSA LPLDLLNNAI TAFSTLEDLI

201 RYLEPERWQL DLEDLYRPTW QLLGKAFVFG RKSRVVDLNL LTEEVRLYSC

251 TPRNFSVSIR EELKRTDTIF WPGCLLVKRC GGNCACCLHN CNECQCVPSK

301 VTKKYHEVLQ LRPKTGVRGL HKSLTDVALE HHEECDCVCR GSTGG

FIG. 11. **Alignment of VEGF-X with Other VEGFs**

```
                             *        20         *        40         *
VEGF_HUMAN  : -------------------------------------------------- :   -
PLGF_HUMAN  : -------------------------------------------------- :   -
VEGB_HUMAN  : -------------------------------------------------- :   -
VEGC_HUMAN  : -------------------------------------------------- :   -
VEGD_HUMAN  : -------------------------------------------------- :   -
990126vegx  : MSLFGLLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERII :  50

                        60         *        80         *       100
VEGF_HUMAN  : -------------------------------------------------- :   -
PLGF_HUMAN  : -------------------------------------------------- :   -
VEGB_HUMAN  : -------------------------------------------------- :   -
VEGC_HUMAN  : -------------------------------------------------- :   -
VEGD_HUMAN  : -------------------------------------------------- :   -
990126vegx  : TVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPE : 100

                             *       120         *       140         *
VEGF_HUMAN  : -------------------------------------------------- :   -
PLGF_HUMAN  : -------------------------------------------------- :   -
VEGB_HUMAN  : -------------------------------------------------- :   -
VEGC_HUMAN  : --------------------MHLLGFFSVACSLLAAALLPGPREAPAAAA :  30
VEGD_HUMAN  : ----------------------------------------MYREWVVVNV :  10
990126vegx  : DDICKYDFVEV--EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE : 148

                       160         *       180         *       200
VEGF_HUMAN  : ------------------------------------------------MN :   2
PLGF_HUMAN  : ------------------------------------------------MP :   2
VEGB_HUMAN  : -------------------------------------------------- :   -
VEGC_HUMAN  : AFESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKM :  80
VEGD_HUMAN  : FMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE :  60
990126vegx  : YFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLED : 198

                             *       220         *       240         *
VEGF_HUMAN  : FLLSWVHWSLALLLYLHHAKWSQAAPMAEGGGQNHHEVVKFMD-VYQRSY :  51
PLGF_HUMAN  : VMRLFPCFLQLLAGLALPAVPPQQWALSAGNGSSEVEVVPFQE-VWGRSY :  51
VEGB_HUMAN  : ---MSPLLRRLLLAALLQLAPAQAPVSQPDAPGHQRKVVSWID-VYTRAT :  46
VEGC_HUMAN  : YKCQLRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQ : 130
VEGD_HUMAN  : DWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQ : 110
990126vegx  : LIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLY : 248

                       260         *       280         *       300
VEGF_HUMAN  : CHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGG---CCND--EGLECVP :  96
PLGF_HUMAN  : CRALERLVDVVSEYPSEVEHMFSPSCVSLLRCTG---CCGD--ENLHCVP :  96
VEGB_HUMAN  : CQPREVVVPLTVELMGTVAKQLVPSCVTVQRCGG---CCPD--DGLECVP :  91
VEGC_HUMAN  : CMPREVCIDVGKEFGVATNTFFKPPCVSVYRCGG---CCNS--EGLQCMN : 175
VEGD_HUMAN  : CSPRETCVEVASELGKSTNTFFKPPCVNVFRCGG---CCNE--ESLICMN : 155
990126vegx  : SCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP : 298
```

FIG. 11 (CONTINUED).

```
                          *        320         *        340         *
VEGF_HUMAN  :  TEESNITMQIMRIKPHQG-----QHIGEMSFLQHNKCECRPKKDRARQEK  :  141
PLGF_HUMAN  :  VETANVTMQLLKIRSGDR-----PSYVELTFSQHVRCECRPLREKMKPER  :  141
VEGB_HUMAN  :  TGQHQVRMQILMIRYPS------SQLGEMSLEEHSQCECRPKKKDSAVKP  :  135
VEGC_HUMAN  :  TSTSYLSKTLFEITVPLSQG---PKPVTISFANHTSCRCMSKLDVYRQVH  :  222
VEGD_HUMAN  :  TSTSYISKQLFEISVPLTSV---PELVPVKVANHTGCKCLPTAPRHPYSI  :  202
990126vegx  :  SKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG---  :  345

                    360         *        380         *        400
VEGF_HUMAN  :  KSVRGKGKGQKRKRKKSRYKSWSVP-------------------------  :  166
PLGF_HUMAN  :  --------------------------------------------------  :    -
VEGB_HUMAN  :  DSPR----------------------------------------------  :  139
VEGC_HUMAN  :  SIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGDDS  :  272
VEGD_HUMAN  :  IRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKCVLQEENPLAGT------  :  246
990126vegx  :  --------------------------------------------------  :    -

                          *        420         *        440         *
VEGF_HUMAN  :  --------------------------------------------------  :    -
PLGF_HUMAN  :  --------------------------------------------------  :    -
VEGB_HUMAN  :  --------------------------------------------------  :    -
VEGC_HUMAN  :  TDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNK  :  322
VEGD_HUMAN  :  ------------------------------------EDHSHLQEPALCGP  :  260
990126vegx  :  --------------------------------------------------  :    -

                    460         *        480         *        500
VEGF_HUMAN  :  ---------CGPCSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNER  :  206
PLGF_HUMAN  :  ---------CGDAVPRR---------------------------------  :  149
VEGB_HUMAN  :  ----------PLCPRCTQHHQRPDPRTCRCRCRRRSFLRCQGRGLELNPD  :  179
VEGC_HUMAN  :  LFPSQCGANREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLK  :  372
VEGD_HUMAN  :  HMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHPD  :  310
990126vegx  :  --------------------------------------------------  :    -

                          *        520         *        540         *
VEGF_HUMAN  :  TCRCDKPRR-----------------------------------------  :  215
PLGF_HUMAN  :  --------------------------------------------------  :    -
VEGB_HUMAN  :  TCRCRKLRR-----------------------------------------  :  188
VEGC_HUMAN  :  GKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCRCVPSYWKRPQMS---  :  419
VEGD_HUMAN  :  TCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP------  :  354
990126vegx  :  --------------------------------------------------  :    -
```

FIG. 12. **Variant Polypeptide Sequences**

```
                  *        20         *        40         *
FL_seq   : MSLFGLLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERII :  50
clone41  : MSLFGLLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERII :  50
clone20  : MSLFGLLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERII :  50

                 60         *        80         *       100
FL_seq   : TVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPE : 100
clone41  : TVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPE : 100
clone20  : TVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPE : 100

                  *       120         *       140         *
FL_seq   : DDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYF : 150
clone41  : DDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYF : 150
clone20  : DDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYF : 150

               160         *       180         *       200
FL_seq   : PSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLI : 200
clone41  : PSEPSNRGGKIIQLHTS--------------------------------- : 167
clone20  : PSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLI : 200

                  *       220         *       240         *
FL_seq   : RYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSC : 250
clone41  : -------------------------------------------------- :   -
clone20  : RYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTE------- : 243

               260         *       280         *       300
FL_seq   : TPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK : 300
clone41  : -------------------------------------------------- :   -
clone20  : -------------------------------------------------- :   -

                  *       320         *       340
FL_seq   : VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG : 345
clone41  : --------------------------------------------- :   -
clone20  : ------EVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG : 282
```

FIG. 13. **Primers for Expression of VEGF-X**

E.coli expression of domain-

vegx-6	AATTGGATCCGAGAGTGGTGGATCTGAACC
vegx-7	AATTGGATCCGGGAAGAAAATCCAGAGTGG
vegx-8	GGTTGAATTCATTATTTTTTAGTAACTTTGCTTGGGACAC
vegX-9	AATTGAATTCATTATCCTCCTGTGCTCCCTC

Baculovirus/insect cell expression of full-length protein-

vegbac1
AATTGGATCCGGAGTCTCACCATCACCACCATCATGAATCCAACCTGAGTAGTAAATTC
C

vegbac2 AATTGAATTCGCTATCCTCCTGTGCTCCCTCTGC

FIG. 14.

>3993180H1 LUNGNON03 INCYTE
CACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGNGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCC
GCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCAT
CCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAG
AATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCTAAAGGACAGGAGAANAGGTCTT
>3510192H1 CONCNOT01 INCYTE
TGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTT
TCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAG
GAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTATTAAATAGATCACCAGCTAGTT
TCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTT
>2559870H1 ADRETUT01 INCYTE
CACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGCACCA
TGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGGGGATAGCCGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGC
AGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCA
TCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGA
>3979767H1 LUNGTUT08 INCYTE
GGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGC
GTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAG
ACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTG
GAAAGAANATTAAATGTTGTATTAAATAGACACCAGCT
>3980011H1 LUNGTUT08 INCYTE
GGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGC
GTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTTACATGCATTCTGAAAGAGGAGA
CATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGG
AAAGAAAATTAAATGTTGTATTAAATAGATCACCA
>4825396H1 BLADDIT01 INCYTE
GAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTCTCCACAATT
GCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTC
AGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGG
AGGATAGCCGCATCACCACCA
>3073703H1 BONEUNT01 INCYTE
AGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGT
GTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACT
GTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCCTTCAG
TTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCA
>1302516H1 PLACNOT02 INCYTE
AGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCCTTCTGAACCTTCTAACAGAGGAGGTAAGATTATAC
AGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCT
CCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTCTCCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTT
ACTAAAAAATACCACGAGGTCC
>3684109H1 HEAANOT01 INCYTE
ATTTCATCTTCAGGATTTACAGTGCATTCTGAAANAGGAGAAATCAAACANAATTAGGAGTTGTGCAACAGCTCTTTTGA
GAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAANAAAATTAAATGTTGTATTAAATAGATCACCAGCTA
GTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAG
TACAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTT
>4713188H1 BRAIHCT01 INCYTE
CAAAGTTACTAAAAAATACCACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCACCG
ACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCAG
CTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGT
TTGCT
>458823H1 KERANOT01 INCYTE
ANGAGTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTT
GTTTGNTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTG
CAACAGCTCTTTTGAGAGGAGGCCTAAAGGNCAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTATTAA
ATAGATC
>1303909H1 PLACNOT02 INCYTE
AGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCCTTCTGAACCTTCTAACAGAGGAGGTAAGATTATAC
AGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCT
CCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAG

FIG. 14 (CONTINUED).

>2739211H1 OVARNOT09 INCYTE
GTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGA
GAAAAGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACG
TATTCCACTAGCTGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAAACTGTGCAA
GTGAGCACCTGAT
>3325591H1 PTHYNOT03 INCYTE
TGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTATT
AAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTCAGTTCTTTCGATACG
GCTTAGGGTAATGTCAGTACAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACCCTAAAGCNCC
ATGTCNNGGGCNAAAANCGAAAAAT
>3733565H1 SMCCNOS01 INCYTE
CCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGNAAGANGAGACATCAAACAG
AATTAGGNGTTGTGCAAAAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTNCAATCGTGGAAAGNAAATT
AAATGTTGTATNAAATNGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGNCNGTATTCAGTCT
TTCGGAACGGCTTAGGGTAATGTCAGTACAGGANAAAAACTGTGCAGTGAG
>3554223H1 SYNONOT01 INCYTE
ATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTCAGTTCTTTCGAT
ACGGCTTAGGGTAATGTCAGTACAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGGCTTAACTCTAAAG
CTCCATGTCCTGGGCCTAAAATCGTATAAAATCTGGATTTTTTTNTTTTTTTTTGCGCATATTCACATATGTAAACCAGN
ACATTCTATGTACNACAAACCTGGTTTTTAAAAAGGAAC
>4507477H1 OVARTDT01 INCYTE
GGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAAT
GTCAGTACAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGGCC
TAAAATCGTATAAAATCTGGA
>4163378H1 BRSTNOT32 INCYTE
AATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGNTCTGTATTTCAGTTCCTTTCGATACG
GCTTAGGGTAATGTCAGTACAGGAAAAAAGCTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCC
ATGTCCTGGGCCTAAAATCGTATA

FIG. 15. 22/54

>2054675H1 BEPINOT01 INCYTE
AAAGGAACTATGTTGCTATGAATTAAACTTGTGTCGTGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAAAATT
TCTGCCATTTAGAAGAAGAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTT
TATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAA
TCTTGTTAAATATATCTATTTTTACCAAAGGTATTTAATATTCTTTTTA
>3993180H1 LUNGNON03 INCYTE
CACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGNGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCC
GCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCAT
CCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAG
AATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCTAAAGGACAGGAGAANAGGTCTT
>3510192H1 CONCNOT01 INCYTE
TGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTT
TCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAG
GAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTATTAAATAGATCACCAGCTAGTT
TCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTT
>4164633H1 BRSTNOT32 INCYTE
CTTGTTAAATATATCTATTTTTACCAAAGGTATTTAATATTCTTTANTTATGACAACTTAGATCAACTATTTTTAGCTTG
GTAAATTTTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATG
TATTTCATTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCA
AAGACTTTTTGANAATAATTAAATTATCATATCTTCCATTCCTGTTATTGGGGGAGAAAAT
>2559870H1 ADRETUT01 INCYTE
CACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGCACCA
TGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGGGGATAGCCGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGC
AGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCA
TCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGA
>3817470H1 BONSTUT01 INCYTE
TTAAAAAGGAACTATGTTGCTATGAATTAAACTTGTGTCATGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAA
AATTTCTGCCATTTAGAAGAAGAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTC
ACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTC
TAATCTGTTAAATATATCTATTTTTACCAAAGGTATTTAATATTCTTT
>3979767H1 LUNGTUT08 INCYTE
GGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGC
GTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAG
ACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTG
GAAAGAANATTAAATGTTGTATTAAATAGACACCAGCT
>3980011H1 LUNGTUT08 INCYTE
GGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGC
GTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTTACATGCATTCTGAAAGAGGAGA
CATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGG
AAAGAAAATTAAATGTTGTATTAAATAGATCACCA
>4825396H1 BLADDIT01 INCYTE
GAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTCTCCACAATT
GCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTC
AGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGG
AGGATAGCCGCATCACCACCA
>3073703H1 BONEUNT01 INCYTE
AGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGT
GTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACT
GTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCCTTCAG
TTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCA
>862169H1 BRAITUT03 INCYTE
AGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCATTCTCGTATGGTGCTAGAGTTAGATTAATCTGCA
TTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAAGACTTTTTGAAAATAATTAAATTATCATATCTTCCATTC
CTGTTATTGGAGATGAAAATAAAAAGCAACTTATGAAAGTAGACATTCAGATCCAGCCATTACTAACCTATTCCTTTTTT
CGGCAAATCTGAGCCTAGC
>4201385H1 BRAITUT29 INCYTE
TTTTTAAAAAGGAACTATGTTGCTATGAATTAAACTTGTGTCGTGCTGATAGGACAGACTGGATTTTTCATATTTCTTAT
TAAAATTTCTGCCATTTAGAAGAAGAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGTGGCCTATCT
TCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTTATATTCTCCTTTGACATATAACTGTTGGCTTTT

09/869198

FIG. 15 (CONTINUED 1). 23/54

CTAATCTGTTAAATATATCTATTTTTACCAAAGGTATTTAATAT
>1302516H1 PLACNOT02 INCYTE
AGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCCTTCTGAACCTTCTAACAGAGGAGGTAAGATTATAC
AGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCT
CCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTCTCCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTT
ACTAAAAAATACCACGAGGTCC
>3684109H1 HEAANOT01 INCYTE
ATTTCATCTTCAGGATTTACAGTGCATTCTGAAANAGGAGAAATCAAACANAATTAGGAGTTGTGCAACAGCTCTTTTGA
GAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAANAAAATTAAATGTTGTATTAAATAGATCACCAGCTA
GTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAG
TACAGGAAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTT
>2549720H1 LUNGTUT06 INCYTE
TTAGCTTGGNAAATTTTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAA
AATACATGTATTTCATTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGT
AAGTTGCAAAGACTTTTTGAAAATAATTAAATTATCATATCTTCCATTCCTGTTATTGGAGATGAAAATAAAAAGCAACT
TATGANAGTAG
>877279H1 LUNGAST01 INCYTE
CTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAAATTTTTCTAAACACAATTGTTATAGCCAGAGGAACAAA
GATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCATTCTCGTATGGTGCTAGAGTTAGATTAATCTGCAT
TTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAAGGCTTTTTGAAAATAATTAAATTATCATATCTTCCATTCC
TGTTATTGGNGG
>4713188H1 BRAIHCT01 INCYTE
CAAAGTTACTAAAAAATACCACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCACCG
ACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCAG
CTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGT
TTGCT
>2171082H1 ENDCNOT03 INCYTE
AGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTTA
TATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCTATTTTTACCAAAGGTATTTAATATT
CTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAAATTTTTCTAAACACAATTGTTATAGCCAGAGGAACAAA
GATGA
>875860H1 LUNGAST01 INCYTE
CTGGATTTTTCATATTTCTTATTAAAATTTCTGCCATTTAGAAGAAGAGAACTACATTCATGGTTTGGAAGAGATAAACC
TGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTTATATTCTCCT
TTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCTATTTTTACCAAAGGTATTTAATATTCTTTTTTAT
GAC
>706168H1 SYNORAT04 INCYTE
GCTCATATTCACATATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGANCTATGTTGCTATGAAT
TAAACTTGTGTCGTGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAAAATTTCTGCCATTTAGAAGAAGAGAAC
TACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCANTTTATCGATAAGTCAGTTTATTTGT
TTCA
>458823H1 KERANOT01 INCYTE
ANGAGTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTT
GTTTGNTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTG
CAACAGCTCTTTTGAGAGGAGGCCTAAAGGNCAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTATTAA
ATAGATC
>538436H1 LNODNOT02 INCYTE
AAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCATTCTCGTATGGTGCTAGAGTTAGATTAATCTG
CATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAAGACTTTTTGAAAATAATTAAATTATCATATCTTCCAT
TCCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGAAAGTAGACATTCAGATCCAGCCATTACTAACCTAT
>1303909H1 PLACNOT02 INCYTE
AGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCCTTCTGAACCTTCTAACAGAGGAGGTAAGATTATAC
AGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCT
CCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAG
>2739211H1 OVARNOT09 INCYTE
GTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGA
GAAAAGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACG
TATTCCACTAGCTGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAAACTGTGCAA
GTGAGCACCTGAT

09/869198

FIG. 15(CONTINUED 2). 24/54

>2550343H1 LUNGTUT06 INCYTE
TGTACATTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCNAATCTTGTTAAATATATCTATTTTTACCAAAG
GTATTTAATATTCTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAAATTTTTCTAAACACAATTGTTATAGC
CAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCATTCTCGTATGGTGCTA
>5321148H1 FIBPFEN06 INCYTE
CACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGNCAAAAATACATGTATTTCATTCTCGTA
TGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAAGACTTTTTGAAAA
TAATTAAATTATCATATCTTCCATTCCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGAAAGTAAATTCAGATCCAC
CATTACTAAC
>879495H1 THYRNOT02 INCYTE
ATTTCATTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAA
AGACTTTTTGAAAATAATTAAATTATCATATCTTCCATTCCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGAAAGT
AGACATTCAGATCCAGCCATTACTAACCTATTCCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGCACCT
TGAAAAA
>3325591H1 PTHYNOT03 INCYTE
TGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTATT
AAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTCAGTTCTTTCGATACG
GCTTAGGGTAATGTCAGTACAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACCCTAAAGCNCC
ATGTCNNGGGCNAAAANCGAAAAAT
>543890H1 OVARNOT02 INCYTE
TTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCA
TTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGNATAGAATTGGTAAGTTGCAAAGNCTT
TTTGAAAATAATTAAATTATCATATCTTCCATTCCTGTTATTGGAGGATGGAAAATAAAAAGCAACTTATGGAAAGTAGG
ACATTCAGATC
>3733565H1 SMCCNOS01 INCYTE
CCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGNAAGANGAGACATCAAACAG
AATTAGGNGTTGTGCAAAAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTNCAATCGTGGAAAGNAAATT
AAATGTTGTATNAAATNGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGNCNGTATTCAGTCT
TTCGGAACGGCTTAGGGTAATGTCAGTACAGGANAAAAACTGTGCAGTGAG
>4641939H1 PROSTMT03 INCYTE
GTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAAACTTGTGTCCATGCTGATAGGACAGACTGGAT
TTTNCATATTTCTTATTAAAATTTCTGCCATTTAGAAGAAGAGAACTACATTCATGGTTTGGNAGAGATAAACCTGAAAA
GAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATGTGTACATTTTTATATTCTCCTTTGACAT
ATAACGTGGCTTT
>2007780H1 TESTNOT03 INCYTE
TTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCTATTTTTACCAAAGGTATTTAAT
ATTCTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAAATTTTTCTAAACACAATTGTTATAGCCAGAGGAAC
AAAGATGATATAAAATATTGTTGCTCTGANAAAAATACATGTAT
>3085331H1 HEAONOT03 INCYTE
GCTCATATTCACATATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATTTGCTATGAATT
AAACTTGTGTCGTGCTGATAGGACAGACTGGNTTTTTCATATTTCTTATTANAATTTCTGCCATTAGAAGAAGAGAACTA
CATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGTGGCCTATTTCACTTTATCGATAAGTCAGT
>3414043H1 PTHYNOT04 INCYTE
GCTCATATTCACATATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT
TAAACTTGTGTCGTGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAAAATTTCTGCCATTTAGAAGAAGAGAAC
TACATTCATGGTTTGGAAGAGATAAACCTGAAA
>3705963H1 PENCNOT07 INCYTE
ANACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGGCCTAAAATCGTATAAAA
TCTGGAnnnnnnnnnnnnnnnnnnnGCTCATATTCACATATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTA
AAAAGGAACTATGTTGCTATGAATTAAACTTGTGTCGTGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAAAAT
TTCTGCCATTAGAAGAAGAGAACTACNTTCANGGTTTGGAAGAGATAACCCTGAAAAGANGGG
>5137051H1 OVARDIT04 INCYTE
AAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAAGACTNTTTGAAAATAATTAAATTATCATATCTTCCATTCCTGT
TATTGGAGATGAANATAAAAAGCAACTTATGAAAGTAGACATTCAGATCCAGCCATTACTAACCTATTCCTTTTTTGGGG
AAATCTGAGCCTAGCTCAGAAAAACATAAAGCACCTTGAAAAAGACTTGGCAGCTTCCTGATAAAGCGTGCTGTNTGTCA
GTAGGAACACATCCTATTTATTGTGATGNTGTGGTTTATTAT
>3554223H1 SYNONOT01 INCYTE
ATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTCAGTTCTTTCGAT
ACGGCTTAGGGTAATGTCAGTACAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGGCTTAACTCTAAAG

09/869198

25/54

FIG. 15 (CONTINUED 3).

CTCCATGTCCTGGGCCTAAAATCGTATAAAATCTGGATTTTTTTNTTTTTTTTTGCGCATATTCACATATGTAAACCAGN
ACATTCTATGTACNACAAACCTGGTTTTTAAAAAGGAAC
>4507477H1 OVARTDT01 INCYTE
GGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAAT
GTCAGTACAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGGCC
TAAAATCGTATAAAATCTGGA
>1955646H1 CONNNOT01 INCYTE
TGGTAAGTTGCAAAGACTTTTTGAAAATAATTAAATTATCATATCTTCCATTCCTGTTATTGGAGATGAAAATAAAAAGC
AACTTATGAAAGTAGACATTCAGATCCAGCCATTACTAACCTATTCCTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAA
ACATAAAGCACCTTGAAAAAGACTTGGCAGCTTCCTGATAAAGCGTGCTGTGCTGTGCAGTAGGGAACACATCCTATTTA
TTGTGATGTTGTGGTTTATATCCTAAACC
>4163378H1 BRSTNOT32 INCYTE
AATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGNTCTGTATTTCAGTTCCTTTCGATACG
GCTTAGGGTAATGTCAGTACAGGAAAAAAGCTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCC
ATGTCCTGGGCCTAAAATCGTATA
>5095141H1 EPIMNON05 INCYTE
AGATAAACCTGAAAAGAAGAGTGGCCTTATNTTCACTTTATCGATAAGTCAGNTTATTTGTTTCATTGTGTACATTTNNA
TATTCTCCTTTTGACATTATAACTGNTGGCTTTTCTAANCNTGTTAAATATATCTATTTTTACCAAAGGTATTTAATATT
CTTT
>943826H1 ADRENOT03 INCYTE
TATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAAGACTTTTTGAA
AATAATTAAATTATCATATCTTCCATTCCTGTTATTGGAGATGAAAATAAAAAGCAACTTATG
>3451273H1 UTRSNON03 INCYTE
TTTTTTNTTTTGCTCATATTCACATATGTAAACCNGAACATTCTATGTACNACAAACCTGGTTTTTAAAAAGGAACTATG
TTGCTATGAATTAAACTTGTGTCGTGCTGATAGGACAGACTGGATTTTTCANATTTCTTANTAANNTTTCTGCCATTTAG
AAGA
>1402278H1 LATRTUT02 INCYTE
GTACAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGGCCTAAA
ATCGTATAAAATCTGGAnnnnnnnnnnnnnnnnnnGCTCATATTCACATATGTAAACCAGAACATTCTATGTACTACAAA
CCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAAACTTGTGTCGTGCTGATAGGACAGACTGGATTTTTCATATTT
CTTA
>4361191H1 SKIRNOT01 INCYTE
GCAAAGACTTTTTGANAATNATTAANTTATCATATCTTCCATTCCTGTTATNGGAGATGANAATAAAAAGCAACTTATGA
AAGTAGACATTCAGATCCAGCCATTACTAACCTATTCCTTTTTGGGGAAATCTGAGCCTAGCNCAGAAAAACATAAAGC
ACCTTGAAAAAGACTTGGCAGCTTCCTGATAAAGCGTGCTGTGCTGTGCAGTAGGAACACATCCNATTTATTGTGNTGTN
GNGGTTTATGATC
>1307017H1 PLACNOT02 INCYTE
TGTCAGTACAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGGC
CTAAAATCGTATAAAATCTGGAnnnnnnnnnnnnnnnnnnGCTCATATTCACATATGTAAACCAGAACATTCTATGTACT
ACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAAACTTGTGTCATGCTGATAGGACAGACTGGATTTTTCA
TAT
>5032225H1 HEARFET03 INCYTE
AATTATCATATCTTCCATTCCTGTTATTGGAGATGNAAATAAAAAGCAACTTATGAAAGTAGACATTCAGATCCAGCCAT
TACTAACCTATTCCTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGCACCTTGAAAAAGACTGTCAGCTTC
CTGATAAAGCGTGCTGTGCTGTGCAGTAGGAACACATCCTATTTATTGTGATGTTGTGGTTTTATTATCTTAAACTCGTT
CCAT
>3732621H1 SMCCNOS01 INCYTE
ANAGATGATATAAAANATTGTTGCTCTGACAANNATACATGTATTTCATTCTCGTATGGTGCTAGAGTTAGATTAATCTG
CNTTTTAAAAAACTGANTTGGAATAGANTTGGTAAGTTGCAAAGNCNTTTGAAAATNATTAAGTTATCAGAT
>3530274H1 BLADNOT09 INCYTE
TTCCATTCCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGAAAGTAGACATTCAGATCCAGCCATTACTAACCTATT
CCTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGCACCTTGAAAAAGACTTGGCAGCTTCCTGATAAAGCG
TGCTGTGCTGTGCAGTAGGAACACATCCTATTTATTGTGATGTTGTGGTTTTATTATCTAAACTCTGTTCCATACACTTG
TATAAATACATGGATATTTTTATGTACAGAAGTATGTCTCTTAACCAGTTCA
>3530249H1 BLADNOT09 INCYTE
CTTCCATTCCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGANAGTAGACATTCAGATCCAGCCATTACTAACCTAT
TCCTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGCACCTTGAAAAAGACTTGGCAGCTTCCTGATAAAGC
GTGCTGTGCTGTGCAGTAGGAACACATCCTATTTATTGTGATGTTGTGGTTTTATTATCTTAAACTCTGTTCCATACACT
TGTATAAATACATGGATATTTTTATGTACAGAAGTATGTCTCTTAACCAGTTCACTTATTGTACCTGG

09/869198

FIG. 16.

VEGFE1	AAAATGTATGGATACAACTTAC	22
VEGFE2	GTTTGATGAAAGATTTGGGCTTG	23
VEGFE3	TTTCTAAAGGAAATCAAATTAG	22
VEGFE4	GATAAGATTTGTATCTGATG	20
VEGFE5	GATGTCTCCTCTTTCAG	17
VEGFE6	GCACAACTCCTAATTCTG	18
VEGFE7	AGCACCTGATTCCGTTGC	19
VEGFE8	TAGTACATAGAATGTTCTGG	20
VEGFE9	AAGAGACATACTTCTGTAC	19
VEGFE10	CCAGGTACAATAAGTGAACTG	21

FIG. 17.

```
      +3                                                 M  N  I   F  L  L
N  L  L  T   E  E  V   R  L  Y
                                                       ]------------------
--------------------------------
       1  AGGAAATCAA ATTAGGATAA GATTTGTATC TGATGAATAT TTTCCTTCTG
AACCTTCTAA CAGAGGAGGT AAGATTATAC
          TCCTTTAGTT TAATCCTATT CTAAACATAG ACTACTTATA AAAGGAAGAC
TTGGAAGATT GTCTCCTCCA TTCTAATATG

      +3  S  C  T  P   R  N  F   S  V  S   I  R  E  E   L  K  R
T  D  T   I  F  W  P   G  C  L
          -------------------------]----------------------------
--------------------------------
      81  AGCTGCACAC CTCGTAACTT CTCAGTGTCC ATAAGGGAAG AACTAAAGAG
AACCGATACC ATTTTCTGGC CAGGTTGTCT
          TCGACGTGTG GAGCATTGAA GAGTCACAGG TATTCCCTTC TTGATTTCTC
TTGGCTATGG TAAAAGACCG GTCCAACAGA
      -2                                                   <-----
--------------------------------

      +3  L  V  K   R  C  G  G   N  C  A   C  C  L   H  N  C  N
E  C  Q   C  V  P   S  K  V
          ------------------------------------------------------
--------------------------------
     161  CCTGGTTAAA CGCTGTGGTG GGAACTGTGC CTGTTGTCTC CACAATTGCA
ATGAATGTCA ATGTGTCCCA AGCAAAGTTA
          GGACCAATTT GCGACACCAC CCTTGACACG GACAACAGAG GTGTTAACGT
TACTTACAGT TACACAGGGT TCGTTTCAAT
      -2  ------------------------------------------------------
--------------------------------

      +3 T  K  K  Y   H  E  V   L  Q  L  R   P  K  T   G  V  R
G  L  H  K   S  L  T   D  V  A
          ------------------------------------------------------
--------------------------------
      +1                                                 V  S  G
D  C  T   N  H  S  P   T  W  P
                                                       ]--------
--------------------------------
     241  CTAAAAAATA CCACGAGGTC CTTCAGTTGA GACCAAAGAC CGGTGTCAGG
GGATTGCACA AATCACTCAC CGACGTGGCC
          GATTTTTTAT GGTGCTCCAG GAAGTCAACT CTGGTTTCTG GCCACAGTCC
CCTAACGTGT TTAGTGAGTG GCTGCACCGG
      -2  ------------------------------------------------------
--------[

      +3  L  E  H  H   E  E  C   D  C  V   C  R  G  S   T  G  G
```

FIG. 17(CONTINUED).

```
                ------------------------------------------------------------
>
     +2                                     V   Q  R  E   H  R  R
I  A  A  S   P  P  A   A  L  A
                                           ]-----------------------
--------------------------------
     +1   W  S  T   M  R  S  V   T  V  C   A  E  G   A  Q  E  D
S  R  I   T  T  S   S  S  C
                ------------------------------------------------------------
--------------------------------
    321  CTGGAGCACC ATGAGGAGTG TGACTGTGTG TGCAGAGGGA GCACAGGAGG
ATAGCCGCAT CACCACCAGC AGCTCTTGCC
         GACCTCGTGG TACTCCTCAC ACTGACACAC ACGTCTCCCT CGTGTCCTCC
TATCGGCGTA GTGGTGGTCG TCGAGAACGG

     +2  Q  S  C  A   V  Q  W   L  I  L   L  E  N  V   C  V  I
S  I  L   N  L  S  C   L  L  Q
                ------------------------------------------------------------
--------------------------------
     +1 P  E  L  C   S  A  V   A  D  S  I   R  E  R   M  R  Y
L  H  P
                ------------------------------------------------------------
-------->
    401  CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAACG TATGCGTTAT
CTCCATCCTT AATCTCAGTT GTTTGCTTCA
         GTCTCGACAC GTCACGTCAC CGACTAAGAT AATCTCTTGC ATACGCAATA
GAGGTAGGAA TTAGAGTCAA CAAACGAAGT

     +2   G  P  F   I  F  R  I   Y  S  A   F
                ------------------------------------>
    481  AGGACCTTTC ATCTTCAGGA TTTACAGTGC ATTCTGAAAG AGGAGACATC
AAACAGAATT AGGAGTTGTG CAACAGCTCT
         TCCTGGAAAG TAGAAGTCCT AAATGTCACG TAAGACTTTC TCCTCTGTAG
TTTGTCTTAA TCCTCAACAC GTTGTCGAGA

    561  TTTGAGAGGA GGCCTAAAGG ACAGGAGAAA AGGTCTTCAA TCGTGGAAAG
AAAATTAAAT GTTGTATTAA ATAGATCACC
         AAACTCTCCT CCGGATTTCC TGTCCTCTTT TCCAGAAGTT AGCACCTTTC
TTTTAATTTA CAACATAATT TATCTAGTGG

    641  AGCTAGTTTC AGAGTTACCA TGTACGTATT CCACTAGCTG GGTTCTGTAT
TTCAGTTCTT TCGATACGGC TTAGGGTAAT
         TCGATCAAAG TCTCAATGGT ACATGCATAA GGTGATCGAC CCAAGACATA
AAGTCAAGAA AGCTATGCCG AATCCCATTA

    721  GTCAGTACAG GAAAAAAACT GTGCAAGTGA GCACCTGATT CCGTTGCCTT
GGCTTAACTC TAAAGCTCCA TGTCCTGGGC
         CAGTCATGTC CTTTTTTTGA CACGTTCACT CGTGGACTAA GGCAACGGAA
CCGAATTGAG ATTTCGAGGT ACAGGACCCG

    801  CTAAAATCGT ATAAAATCTG GA
         GATTTTAGCA TATTTTAGAC CT
```

FIG. 18.

```
      +3                                         M  N  I   F  L  L
N  L  L  T   E  E  V   R  L  Y
                                                ]------------------
--------------------------------
        1  AGGAAATCAA ATTAGGATAA GATTTGTATC TGATGAATAT TTTCCTTCTG
AACCTTCTAA CAGAGGAGGT AAGATTATAC
           TCCTTTAGTT TAATCCTATT CTAAACATAG ACTACTTATA AAAGGAAGAC
TTGGAAGATT GTCTCCTCCA TTCTAATATG

      +3  S  C  T  P   R  N  F   S  V  S   I  R  E  E   L  K  R
T  D  T   I  F  W  P   G  C  L
           -------------------------]----------------------------
--------------------------------
       81  AGCTGCACAC CTCGTAACTT CTCAGTGTCC ATAAGGGAAG AACTAAAGAG
AACCGATACC ATTTTCTGGC CAGGTTGTCT
           TCGACGTGTG GAGCATTGAA GAGTCACAGG TATTCCCTTC TTGATTTCTC
TTGGCTATGG TAAAAGACCG GTCCAACAGA
      -2                                                    <-----
--------------------------------

      +3   L  V  K   R  C  G  G   N  C  A   C  C  L   H  N  C  N
E  C  Q   C  V  P   S  K  V
           ------------------------------------------------------
--------------------------------
      161  CCTGGTTAAA CGCTGTGGTG GGAACTGTGC CTGTTGTCTC CACAATTGCA
ATGAATGTCA ATGTGTCCCA AGCAAAGTTA
           GGACCAATTT GCGACACCAC CCTTGACACG GACAACAGAG GTGTTAACGT
TACTTACAGT TACACAGGGT TCGTTTCAAT
      -2 ------------------------------------------------------
--------------------------------

      +3 T  K  K  Y   H  E  V   L  Q  L  R   P  K  T   G  V  R
G  L  H  K   S  L  T   D  V  A
           ------------------------------------------------------
--------------------------------
      +1                                                 V  S  G
D  C  T   N  H  S  P   T  W  P
                                                       ]--------
--------------------------------
      241  CTAAAAAATA CCACGAGGTC CTTCAGTTGA GACCAAAGAC CGGTGTCAGG
GGATTGCACA AATCACTCAC CGACGTGGCC
           GATTTTTTAT GGTGCTCCAG GAAGTCAACT CTGGTTTCTG GCCACAGTCC
CCTAACGTGT TTAGTGAGTG GCTGCACCGG
```

FIG. 18 (CONTINUED 1).

```
       -2 --------------------------------------------------------
--------[

       +3 L  E  H  H   E  E  C   D  C  V   C  R  G  S   T  G  G
          --------------------------------------------------------
>
       +2                                    V   Q  R  E   H  R  R
I  A  A  S   P  P  A   A  L  A
                                            ]----------------------
---------------------------------
       +1  W  S  T   M  R  S  V   T  V  C   A  E  G   A  Q  E  D
S  R  I   T  T  S   S  S  C
          --------------------------------------------------------
---------------------------------
     321  CTGGAGCACC ATGAGGAGTG TGACTGTGTG TGCAGAGGGA GCACAGGAGG
ATAGCCGCAT CACCACCAGC AGCTCTTGCC
          GACCTCGTGG TACTCCTCAC ACTGACACAC ACGTCTCCCT CGTGTCCTCC
TATCGGCGTA GTGGTGGTCG TCGAGAACGG

       +2 Q  S  C  A   V  Q  W   L  I  L   L  E  N  V   C  V  I
S  I  L   N  L  S  C   L  L  Q
          --------------------------------------------------------
---------------------------------
       +1 P  E  L  C   S  A  V   A  D  S  I   R  E  R   M  R  Y
L  H  P
          --------------------------------------------------------
-------->
     401  CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAACG TATGCGTTAT
CTCCATCCTT AATCTCAGTT GTTTGCTTCA
          GTCTCGACAC GTCACGTCAC CGACTAAGAT AATCTCTTGC ATACGCAATA
GAGGTAGGAA TTAGAGTCAA CAAACGAAGT

       +2  G  P  F   I  F  R  I   Y  S  A   F
          ------------------------------------->
     481  AGGACCTTTC ATCTTCAGGA TTTACAGTGC ATTCTGAAAG AGGAGACATC
AAACAGAATT AGGAGTTGTG CAACAGCTCT
          TCCTGGAAAG TAGAAGTCCT AAATGTCACG TAAGACTTTC TCCTCTGTAG
TTTGTCTTAA TCCTCAACAC GTTGTCGAGA

     561  TTTGAGAGGA GGCCTAAAGG ACAGGAGAAA AGGTCTTCAA TCGTGGAAAG
AAAATTAAAT GTTGTATTAA ATAGATCACC
          AAACTCTCCT CCGGATTTCC TGTCCTCTTT TCCAGAAGTT AGCACCTTTC
TTTTAATTTA CAACATAATT TATCTAGTGG

     641  AGCTAGTTTC AGAGTTACCA TGTACGTATT CCACTAGCTG GGTTCTGTAT
TTCAGTTCTT TCGATACGGC TTAGGGTAAT
          TCGATCAAAG TCTCAATGGT ACATGCATAA GGTGATCGAC CCAAGACATA
AAGTCAAGAA AGCTATGCCG AATCCCATTA

     721  GTCAGTACAG GAAAAAAACT GTGCAAGTGA GCACCTGATT CCGTTGCCTT
GGCTTAACTC TAAAGCTCCA TGTCCTGGGC
```

FIG. 18 (CONTINUED 2).

CAGTCATGTC CTTTTTTTGA CACGTTCACT CGTGGACTAA GGCAACGGAA CCGAATTGAG ATTTCGAGGT ACAGGACCCG

801 CTAAAATCGT ATAAAATCTG GATTTTTTTN TTTTTTTTTG CGCATATTCA CATATGTAAA CCAGAACATT CTATGTACTA
GATTTTAGCA TATTTTAGAC CTAAAAAAAN AAAAAAAAAC GCGTATAAGT GTATACATTT GGTCTTGTAA GATACATGAT

881 CAAACCTGGT TTTTAAAAAG GAACTATGTT GCTATGAATT AAACTTGTGT CGTGCTGATA GGACAGACTG GATTTTTCAT
GTTTGGACCA AAAATTTTTC CTTGATACAA CGATACTTAA TTTGAACACA GCACGACTAT CCTGTCTGAC CTAAAAAGTA
-3 <---

961 ATTTCTTATT AAAATTTCTG CCATTTAGAA GAAGAGAACT ACATTCATGG TTTGGAAGAG ATAAACCTGA AAAGAAGAGT
TAAAGAATAA TTTTAAAGAC GGTAAATCTT CTTCTCTTGA TGTAAGTACC AAACCTTCTC TATTTGGACT TTTCTTCTCA
-3 --

1041 GGCCTTATCT TCACTTTATC GATAAGTCAG TTTATTTGTT TCATTGTGTA CATTTTTATA TTCTCCTTTT GACATTATAA
CCGGAATAGA AGTGAAATAG CTATTCAGTC AAATAAACAA AGTAACACAT GTAAAAATAT AAGAGGAAAA CTGTAATATT
-3 --------------[

1121 CTGTTGGCTT TTCTAATCTT GTTAAATATA TCTATTTTTA CCAAAGGTAT TTAATATTCT TTTTTATGAC AACTTAGATC
GACAACCGAA AAGATTAGAA CAATTTATAT AGATAAAAAT GGTTTCCATA AATTATAAGA AAAAATACTG TTGAATCTAG

1201 AACTATTTTT AGCTTGGTAA ATTTTTCTAA ACACAATTGT TATAGCCAGA GGAACAAAGA TGATATAAAA TATTGTTGCT
TTGATAAAAA TCGAACCATT TAAAAAGATT TGTGTTAACA ATATCGGTCT CCTTGTTTCT ACTATATTTT ATAACAACGA

1281 CTGACAAAAA TACATGTATT TCATTCTCGT ATGGTGCTAG AGTTAGATTA ATCTGCATTT TAAAAAACTG AATTGGAATA
GACTGTTTTT ATGTACATAA AGTAAGAGCA TACCACGATC TCAATCTAAT TAGACGTAAA ATTTTTTGAC TTAACCTTAT

1361 GAATTGGTAA GTTGCAAAGA CTTTTTGAAA ATAATTAAAT TATCATATCT TCCATTCCTG TTATTGGAGA TGAAAATAAA
CTTAACCATT CAACGTTTCT GAAAAACTTT TATTAATTTA ATAGTATAGA AGGTAAGGAC AATAACCTCT ACTTTTATTT

1441 AAGCAACTTA TGAAAGTAGA CATTCAGATC CAGCCATTAC TAACCTATTC CTTTTTTGGG GAAATCTGAG CCTAGCTCAG
TTCGTTGAAT ACTTTCATCT GTAAGTCTAG GTCGGTAATG ATTGGATAAG GAAAAAACCC CTTTAGACTC GGATCGAGTC

FIG. 18 (CONTINUED 3).

1521 AAAAACATAA AGCACCTTGA AAAAGACTTG GCAGCTTCCT GATAAAGCGT GCTGTGCTGT GCAGTAGGAA CACATCCTAT
TTTTTGTATT TCGTGGAACT TTTTCTGAAC CGTCGAAGGA CTATTTCGCA CGACACGACA CGTCATCCTT GTGTAGGATA

1601 TTATTGTGAT GTTGTGGTTT TATTATCTTA AACTCTGTTC CATACACTTG TATAAATACA TGGATATTTT TATGTACAGA
AATAACACTA CAACACCAAA ATAATAGAAT TTGAGACAAG GTATGTGAAC ATATTTATGT ACCTATAAAA ATACATGTCT

1681 AGTATGTCTC TTAACCAGTT CACTTATTGT ACCTGG
TCATACAGAG AATTGGTCAA GTGAATAACA TGGACC

FIG. 19. **DNA and polypeptide sequence used for mammalian cell expression**

```
  +1            m  s  l  f   g  l  l   l  l  t   s  a  l   a  g  q  r
   1  GGATCCAAAA TGAGCCTCTT CGGGCTTCTC CTGCTGACAT CTGCCCTGGC CGGCCAGAGA

  +1  q  g  t  q   a  E  S   N  L  S   S  K  F  Q   F  S  S   N  K  E
  61  CAGGGGACTC AGGCGGAATC CAACCTGAGT AGTAAATTCC AGTTTTCCAG CAACAAGGAA

  +1  Q  N  G  V   Q  D  P   Q  H  E   R  I  I  T   V  S  T   N  G  S
 121  CAGAACGGAG TACAAGATCC TCAGCATGAG AGAATTATTA CTGTGTCTAC TAATGGAAGT

  +1  I  H  S  P   R  F  P   H  T  Y   P  R  N  T   V  L  V   W  R  L
 181  ATTCACAGCC CAAGGTTTCC TCATACTTAT CCAAGAAATA CGGTCTTGGT ATGGAGATTA

  +1  V  A  V  E   E  N  V   W  I  Q   L  T  F  D   E  R  F   G  L  E
 241  GTAGCAGTAG AGGAAAATGT ATGGATACAA CTTACGTTTG ATGAAAGATT TGGGCTTGAA

  +1  D  P  E  D   D  I  C   K  Y  D   F  V  E  V   E  E  P   S  D  G
 301  GACCCAGAAG ATGACATATG CAAGTATGAT TTTGTAGAAG TTGAGGAACC CAGTGATGGA

  +1  T  I  L  G   R  W  C   G  S  G   T  V  P  G   K  Q  I   S  K  G
 361  ACTATATTAG GGCGCTGGTG TGGTTCTGGT ACTGTACCAG GAAAACAGAT TTCTAAAGGA

  +1  N  Q  I  R   I  R  F   V  S  D   E  Y  F  P   S  E  P   G  F  C
 421  AATCAAATTA GGATAAGATT TGTATCTGAT GAATATTTTC CTTCTGAACC AGGGTTCTGC

  +1  I  H  Y  N   I  V  M   P  Q  F   T  E  A  V   S  P  S   V  L  P
 481  ATCCACTACA ACATTGTCAT GCCACAATTC ACAGAAGCTG TGAGTCCTTC AGTGCTACCC

  +1  P  S  A  L   P  L  D   L  L  N   N  A  I  T   A  F  S   T  L  E
 541  CCTTCAGCTT TGCCACTGGA CCTGCTTAAT AATGCTATAA CTGCCTTTAG TACCTTGGAA

  +1  D  L  I  R   Y  L  E   P  E  R   W  Q  L  D   L  E  D   L  Y  R
 601  GACCTTATTC GATATCTTGA ACCAGAGAGA TGGCAGTTGG ACTTAGAAGA TCTATATAGG

  +1  P  T  W  Q   L  L  G   K  A  F   V  F  G  R   K  S  R   V  V  D
 661  CCAACTTGGC AACTTCTTGG CAAGGCTTTT GTTTTTGGAA GAAAATCCAG AGTGGTGGAT

  +1  L  N  L  L   T  E  E   V  R  L   Y  S  C  T   P  R  N   F  S  V
 721  CTGAACCTTC TAACAGAGGA GGTAAGATTA TACAGCTGCA CACCTCGTAA CTTCTCAGTG

  +1  S  I  R  E   E  L  K   R  T  D   T  I  F  W   P  G  C   L  L  V
 781  TCCATAAGGG AAGAACTAAA GAGAACCGAT ACCATTTTCT GGCCAGGTTG TCTCCTGGTT

  +1  K  R  C  G   G  N  C   A  C  C   L  H  N  C   N  E  C   Q  C  V
 841  AAACGCTGTG GTGGGAACTG TGCCTGTTGT CTCCACAATT GCAATGAATG TCAATGTGTC

  +1  P  S  K  V   T  K  K   Y  H  E   V  L  Q  L   R  P  K   T  G  V
 901  CCAAGCAAAG TTACTAAAAA ATACCACGAG GTCCTTCAGT TGAGACCAAA GACCGGTGTC

  +1  R  G  L  H   K  S  L   T  D  V   A  L  E  H   H  E  E   C  D  C
 961  AGGGGATTGC ACAAATCACT CACCGACGTG GCCCTGGAGC ACCATGAGGA GTGTGACTGT

  +1  V  C  R  G   S  T  G   G  S  R   G  P  F  E   G  K  P   I  P  N
1021  GTGTGCAGAG GGAGCACAGG AGGATCTAGA GGGCCCTTCG AAGGTAAGCC TATCCCTAAC

  +1  P  L  L  G   L  D  S   T  R  T   G  H  H  H   H  H  H
1081  CCTCTCCTCG GTCTCGATTC TACGCGTACC GGTCATCATC ACCATCACCA TTGA
```

FIG. 20. DNA and polypeptide sequence used for baculovirus/insect cell expression


```
   1  GAATTCAAAG GCCTGTATTT TACTGTTTTC GTAACAGTTT TGTAATAAAA AAACCTATAA

  +3   m  k  f   l  v  n   v  a  l   v  f  m   v  v  y   i  s  y  i
  61  ATATGAAATT CTTAGTCAAC GTTGCCCTTG TTTTTATGGT CGTATACATT TCTTACATCT

  +3 y  a  D  P   E  S  H   H  H  H   H  H  E   S  N  L   S  S  K  F
 121  ATGCGGATCC CGAGTCTCAC CATCACCACC ATCATGAATC CAACCTGAGT AGTAAATTCC

  +3 Q  F  S  S   N  K  E   Q  N  G   V  Q  D   P  Q  H   E  R  I  I
 181  AGTTTTCCAG CAACAAGGAA CAGAACGGAG TACAAGATCC TCAGCATGAG AGAATTATTA

  +3 T  V  S  T   N  G  S   I  H  S   P  R  F   P  H  T   Y  P  R  N
 241  CTGTGTCTAC TAATGGAAGT ATTCACAGCC CAAGGTTTCC TCATACTTAT CCAAGAAATA

  +3 T  V  L  V   W  R  L   V  A  V   E  E  N   V  W  I   Q  L  T  F
 301  CGGTCTTGGT ATGGAGATTA GTAGCAGTAG AGGAAAATGT ATGGATACAA CTTACGTTTG

  +3 D  E  R  F   G  L  E   D  P  E   D  D  I   C  K  Y   D  F  V  E
 361  ATGAAAGATT TGGGCTTGAA GACCCAGAAG ATGACATATG CAAGTATGAT TTTGTAGAAG

  +3 V  E  E  P   S  D  G   T  I  L   G  R  W   C  G  S   G  T  V  P
 421  TTGAGGAACC CAGTGATGGA ACTATATTAG GGCGCTGGTG TGGTTCTGGT ACTGTACCAG

  +3 G  K  Q  I   S  K  G   N  Q  I   R  I  R   F  V  S   D  E  Y  F
 481  GAAAACAGAT TTCTAAAGGA AATCAAATTA GGATAAGATT TGTATCTGAT GAATATTTTC

  +3 P  S  E  P   G  F  C   I  H  Y   N  I  V   M  P  Q   F  T  E  A
 541  CTTCTGAACC AGGGTTCTGC ATCCACTACA ACATTGTCAT GCCACAATTC ACAGAAGCTG

  +3 V  S  P  S   V  L  P   P  S  A   L  P  L   D  L  L   N  N  A  I
 601  TGAGTCCTTC AGTGCTACCC CCTTCAGCTT TGCCACTGGA CCTGCTTAAT AATGCTATAA

  +3 T  A  F  S   T  L  E   D  L  I   R  Y  L   E  P  E   R  W  Q  L
 661  CTGCCTTTAG TACCTTGGAA GACCTTATTC GATATCTTGA ACCAGAGAGA TGGCAGTTGG

  +3 D  L  E  D   L  Y  R   P  T  W   Q  L  L   G  K  A   F  V  F  G
 721  ACTTAGAAGA TCTATATAGG CCAACTTGGC AACTTCTTGG CAAGGCTTTT GTTTTTGGAA

  +3 R  K  S  R   V  V  D   L  N  L   L  T  E   E  V  R   L  Y  S  C
 781  GAAAATCCAG AGTGGTGGAT CTGAACCTTC TAACAGAGGA GGTAAGATTA TACAGCTGCA

  +3 T  P  R  N   F  S  V   S  I  R   E  E  L   K  R  T   D  T  I  F
 841  CACCTCGTAA CTTCTCAGTG TCCATAAGGG AAGAACTAAA GAGAACCGAT ACCATTTTCT

  +3 W  P  G  C   L  L  V   K  R  C   G  G  N   C  A  C   C  L  H  N
 901  GGCCAGGTTG TCTCCTGGTT AAACGCTGTG GTGGGAACTG TGCCTGTTGT CTCCACAATT

  +3 C  N  E  C   Q  C  V   P  S  K   V  T  K   K  Y  H   E  V  L  Q
 961  GCAATGAATG TCAATGTGTC CCAAGCAAAG TTACTAAAAA ATACCACGAG GTCCTTCAGT

  +3 L  R  P  K   T  G  V   R  G  L   H  K  S   L  T  D   V  A  L  E
1021  TGAGACCAAA GACCGGTGTC AGGGGATTGC ACAAATCACT CACCGACGTG GCCCTGGAGC

  +3 H  H  E  E   S  D  C   V  C  R   G  S  T   G  G
1081  ACCATGAGGA GTGTGACTGT GTGTGCAGAG GGAGCACAGG AGGATAGCTC TAGA
```

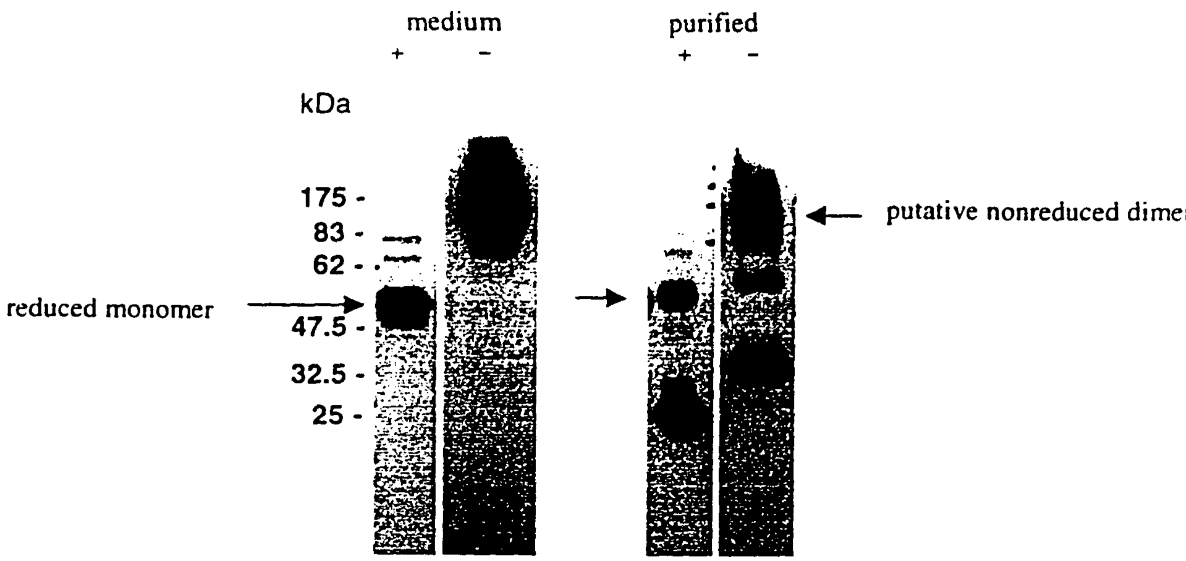
09/869198

FIG. 21. **DNA and polypeptide sequence used for *E.coli* expression** 35/54

```
+3   Q  T  N   S  S  S   N  N  N   N  N  N   N  N  N   L  G  I
1    CGCAGACTAA TTCGAGCTCG AACAACAACA ACAATAACAA TAACAACAAC CTCGGGATCG

+3   E  G  R  I   S  E  F   E  S  N  L   S  S  K   F  Q  F   S  S  N
61   AGGGAAGGAT TTCAGAATTC GAATCCAACC TGAGTAGTAA ATTCCAGTTT TCCAGCAACA

+3   K  E  Q  N   G  V  Q   D  P  Q  H   E  R  I   I  T  V   S  T  N
121  AGGAACAGAA CGGAGTACAA GATCCTCAGC ATGAGAGAAT TATTACTGTG TCTACTAATG

+3   G  S  I  H   S  P  R   F  P  H  T   Y  P  R   N  T  V   L  V  W
181  GAAGTATTCA CAGCCCAAGG TTTCCTCATA CTTATCCAAG AAATACGGTC TTGGTATGGA

+3   R  L  V  A   V  E  E   N  V  W  I   Q  L  T   F  D  E   R  F  G
241  GATTAGTAGC AGTAGAGGAA AATGTATGGA TACAACTTAC GTTTGATGAA AGATTTGGGC

+3   L  E  D  P   E  D  D   I  C  K  Y   D  F  V   E  V  E   E  P  S
301  TTGAAGACCC AGAAGATGAC ATATGCAAGT ATGATTTTGT AGAAGTTGAG GAACCCAGTG

+3   D  G  T  I   L  G  R   W  C  G  S   G  T  V   P  G  K   Q  I  S
361  ATGGAACTAT ATTAGGGCGC TGGTGTGGTT CTGGTACTGT ACCAGGAAAA CAGATTTCTA

+3   K  G  N  Q   I  R  I   R  F  V  S   D  E  Y   F  P  S   E  P  G
421  AAGGAAATCA AATTAGGATA AGATTTGTAT CTGATGAATA TTTTCCTTCT GAACCAGGGT

+3   F  C  I  H   Y  N  I   V  M  P  Q   F  T  E   A  V  S   P  S  V
481  TCTGCATCCA CTACAACATT GTCATGCCAC AATTCACAGA AGCTGTGAGT CCTTCAGTGC

+3   L  P  P  S   A  L  P   L  D  L  L   N  N  A   I  T  A   F  S  T
541  TACCCCCTTC AGCTTTGCCA CTGGACCTGC TTAATAATGC TATAACTGCC TTTAGTACCT

+3   L  E  D  L   I  R  Y   L  E  P  E   R  W  Q   L  D  L   E  D  L
601  TGGAAGACCT TATTCGATAT CTTGAACCAG AGAGATGGCA GTTGGACTTA GAAGATCTAT

+3   Y  R  P  T   W  Q  L   L  G  K  A   F  V  F   G  R  K   S  R  V
661  ATAGGCCAAC TTGGCAACTT CTTGGCAAGG CTTTTGTTTT TGGAAGAAAA TCCAGAGTGG

+3   V  D  L  N   L  L  T   E  E  V  R   L  Y  S   C  T  P   R  N  F
721  TGGATCTGAA CCTTCTAACA GAGGAGGTAA GATTATACAG CTGCACACCT CGTAACTTCT

+3   S  V  S  I   R  E  E   L  K  R  T   D  T  I   F  W  P   G  C  L
781  CAGTGTCCAT AAGGGAAGAA CTAAAGAGAA CCGATACCAT TTTCTGGCCA GGTTGTCTCC

+3   L  V  K  R   C  G  G   N  C  A  C   C  L  H   N  C  N   E  C  Q
841  TGGTTAAACG CTGTGGTGGG AACTGTGCCT GTTGTCTCCA CAATTGCAAT GAATGTCAAT

+3   C  V  P  S   K  V  T   K  K  Y  H   E  V  L   Q  L  R   P  K  T
901  GTGTCCCAAG CAAAGTTACT AAAAAATACC ACGAGGTCCT TCAGTTGAGA CCAAAGACCG

+3   G  V  R  G   L  H  K   S  L  T  D   V  A  L   E  H  H   E  E  C
961  GTGTCAGGGG ATTGCACAAA TCACTCACCG ACGTGGCCCT GGAGCACCAT GAGGAGTGTG

+3   D  C  V  C   R  G  S   T  G  G  H   H  H  H   H  H  *
1021 ACTGTGTGTG CAGAGGGAGC ACAGGAGGAC ATCATCACCA TCACCATTGA TCTAGAGTCG

1081 ACCTGCAGGC AAGCTT
```

FIG. 22. **Disulphide-linked dimerisation of VEGF-X**

(A) Mammalian cell expression



(B) ***E.coli*** **expression**

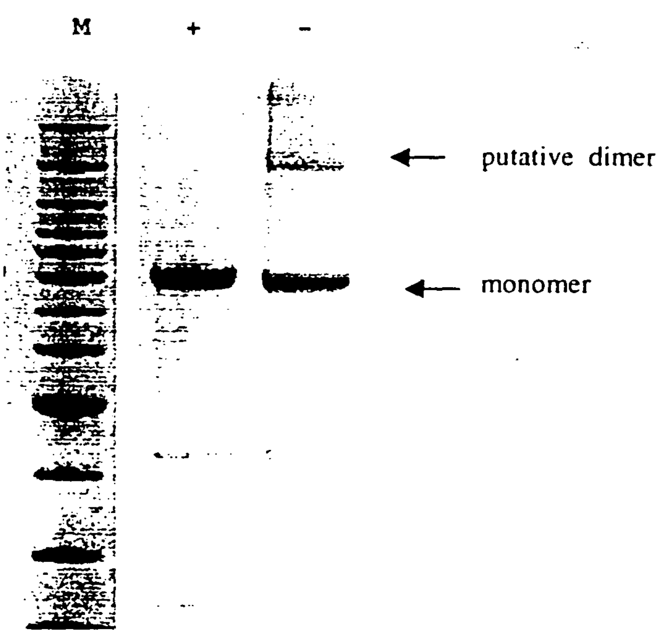


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FIG. 23. **Glycosylation of VEGF-X**

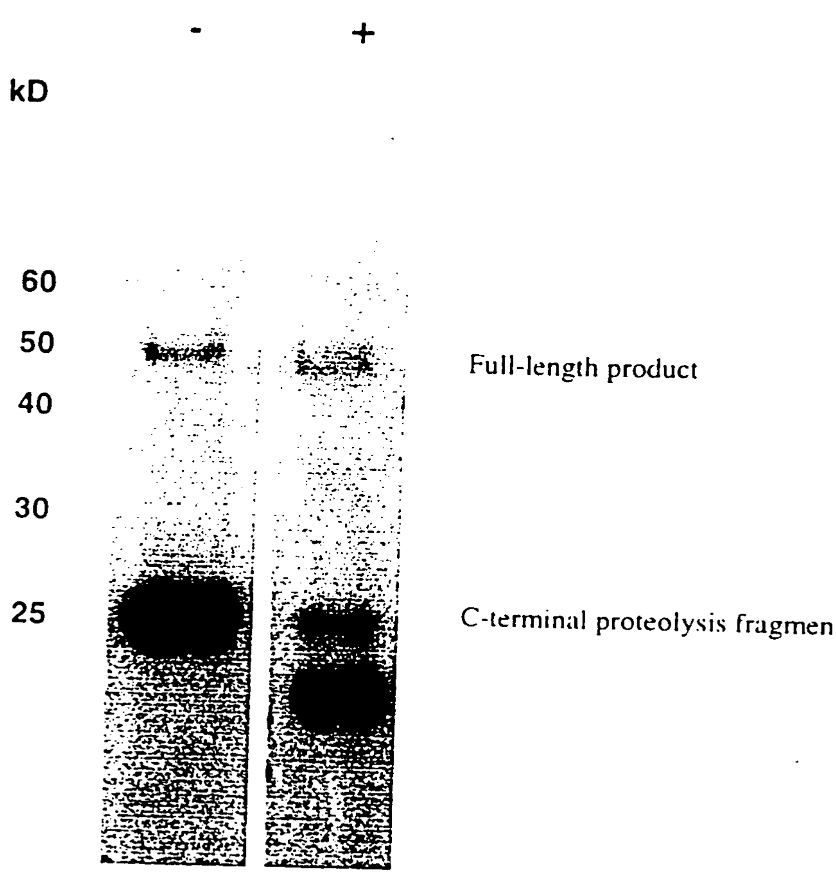

FIG. 24.

DNA and polypeptide sequence used for *E.coli* expression of the PDGF-like domain

```
 +3                 M  R   G  S  H  H   H  H  H   H  G  M   A  S  M
  1   AAGGAGATAT ACATATGCGG GGTTCTCATC ATCATCATCA TCATGGTATG GCTAGCATGA

 +3 T  G  G  Q   Q  M  G   R  D  L  Y   D  D  D   D  K  D   P  G  R
 61   CTGGTGGACA GCAAATGGGT CGGGATCTGT ACGACGATGA CGATAAGGAT CCGGGAAGAA

 +3 K  S  R  V   V  D  L   N  L  L  T   E  E  V   R  L  Y   S  C  T
121   AATCCAGAGT GGTGGATCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC AGCTGCACAC

 +3 P  R  N  F   S  V  S   I  R  E  E   L  K  R   T  D  T   I  F  W
181   CTCGTAACTT CTCAGTGTCC ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTTCTGGC

 +3 P  G  C  L   L  V  K   R  C  G  G   N  C  A   C  C  L   H  N  C
241   CAGGTTGTCT CCTGGTTAAA CGCTGTGGTG GGAACTGTGC CTGTTGTCTC CACAATTGCA

 +3 N  E  C  Q   C  V  P   S  K  V  T   K  K  Y   H  E  V   L  Q  L
301   ATGAATGTCA ATGTGTCCCA AGCAAAGTTA CTAAAAAATA CCACGAGGTC CTTCAGTTGA

 +3 R  P  K  T   G  V  R   G  L  H  K   S  L  T   D  V  A   L  E  H
361   GACCAAAGAC CGGTGTCAGG GGATTGCACA AATCACTCAC CGACGTGGCC CTGGAGCACC

 +3 H  E  E  C   D  C  V   C  R  G  S   T  G  G
421   ATGAGGAGTG TGACTGTGTG TGCAGAGGGA GCACAGGAGG ATAATGAATT CGAAGCTTGA

481   TCCGGCTGCT AACAAAGCCC
```

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FIG. 25. Expression of PDGF domain in *E.coli*

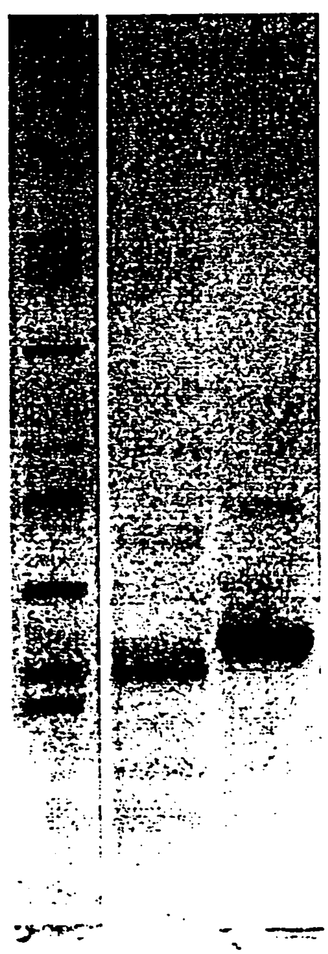

FIG. 26.

DNA and polypeptide sequence used for *E.coli* expression of the CUB-like domain

```
 +2      M  A   M  D  I  G   I  N  S   D  P  E   S  H  H  H   H  H
  1   GGCGATGGCC ATGGATATCG GAATTAATTC GGATCCGGAG TCTCACCATC ACCACCATCA

 +2   E  S  N   L  S  S  K   F  Q  F   S  S  N   K  E  Q  N   G  V  Q
 61   TGAATCCAAC CTGAGTAGTA AATTCCAGTT TTCCAGCAAC AAGGAACAGA ACGGAGTACA

 +2   D  P  Q   H  E  R  I   I  T  V   S  T  N   G  S  I  H   S  P  R
121   AGATCCTCAG CATGAGAGAA TTATTACTGT GTCTACTAAT GGAAGTATTC ACAGCCCAAG

 +2   F  P  H   T  Y  P  R   N  T  V   L  V  W   R  L  V  A   V  E  E
181   GTTTCCTCAT ACTTATCCAA GAAATACGGT CTTGGTATGG AGATTAGTAG CAGTAGAGGA

 +2   N  V  W   I  Q  L  T   F  D  E   R  F  G   L  E  D  P   E  D  D
241   AAATGTATGG ATACAACTTA CGTTTGATGA AAGATTTGGG CTTGAAGACC CAGAAGATGA

 +2   I  C  K   Y  D  F  V   E  V  E   E  P  S   D  G  T  I   L  G  R
301   CATATGCAAG TATGATTTTG TAGAAGTTGA GGAACCCAGT GATGGAACTA TATTAGGGCG

 +2   W  C  G   S  G  T  V   P  G  K   Q  I  S   K  G  N  Q   I  R  I
361   CTGGTGTGGT TCTGGTACTG TACCAGGAAA ACAGATTTCT AAAGGAAATC AAATTAGGAT

 +2   R  F  V   S  D  E  Y   F  P  S   E  P  G   F  C  I  H   Y  N  I
421   AAGATTTGTA TCTGATGAAT ATTTTCCTTC TGAACCAGGG TTCTGCATCC ACTACAACAT

 +2   V  M  P   C  F  T  E   A  V
481   TGTCATGCCA CAATTCACAG AAGCTGTGTA GTCGAGCTCC GTCGACAAGC TTGCGGCCGC

541   ACTCGAGCAC
```

FIG. 27. **Expression of the CUB domain in *E.coli***

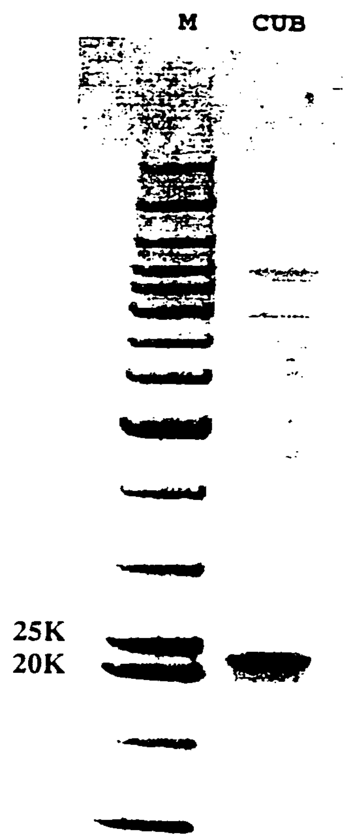

FIG. 28. The Effect of Truncated VEGF-X (CUB domain) on HUVEC Proliferation.

(A)

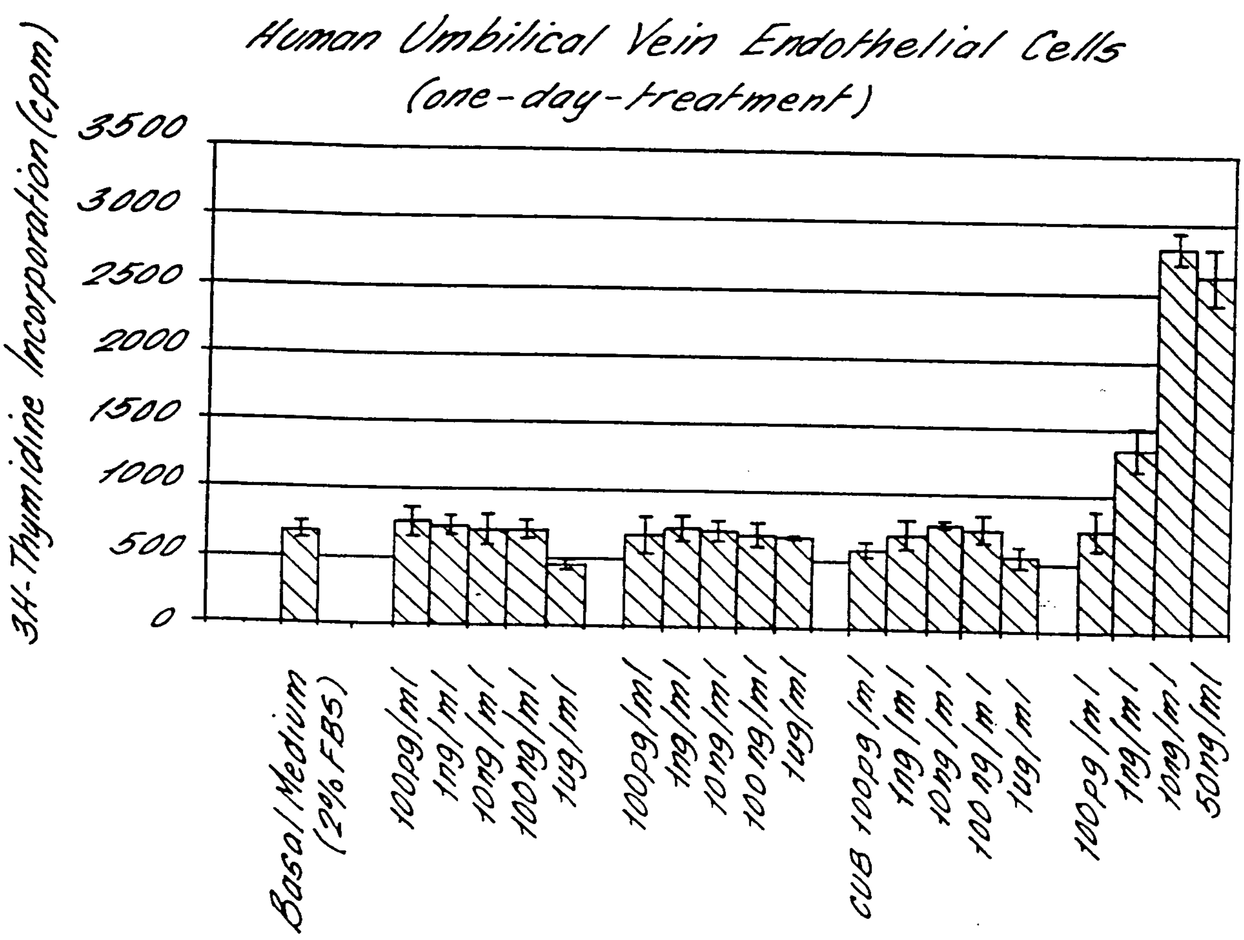

FIG. 28 (CONTINUED 1).

(B)

Human Umbilical Vein Endothelial Cells (24-hour-starving Followed by one-day-treatment)

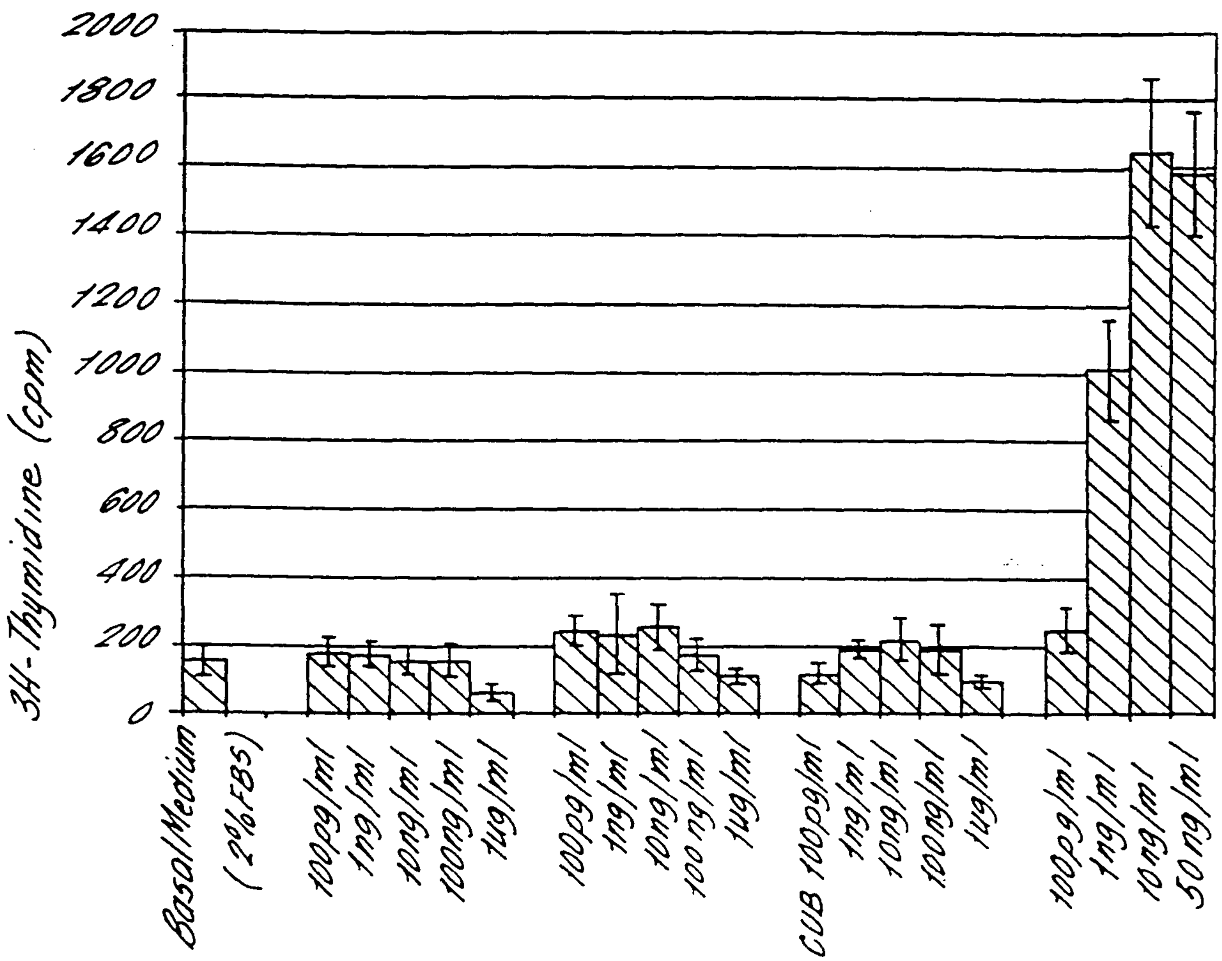

FIG. 28 (CONTINUED 2).

(C)

The effect of VEGF-A_{165} and VEGF-X CUB domain on the proliferation of HUVEC (two-day-treatment).

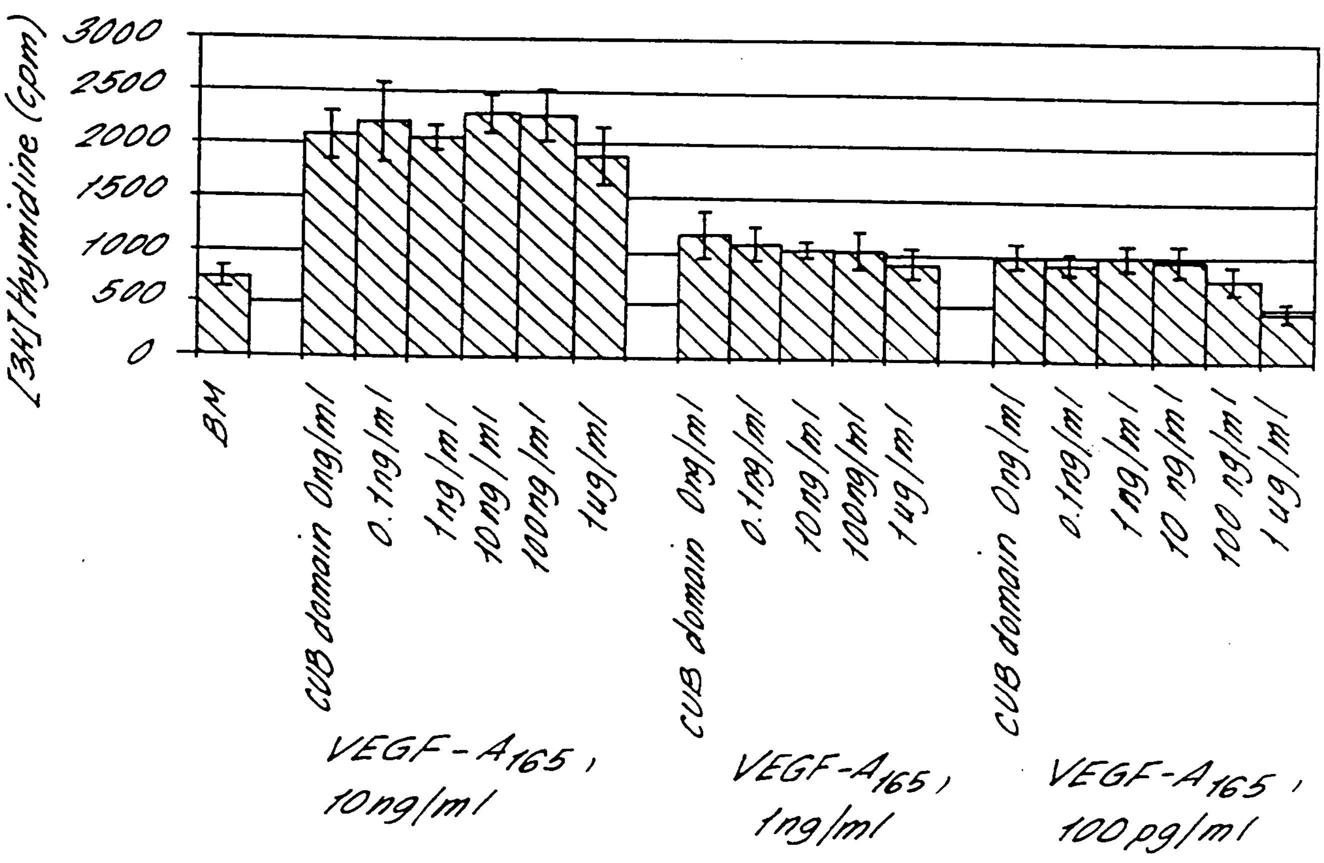

FIG. 29.

Tissue distribution of mRNA

(A) - Normal tissues

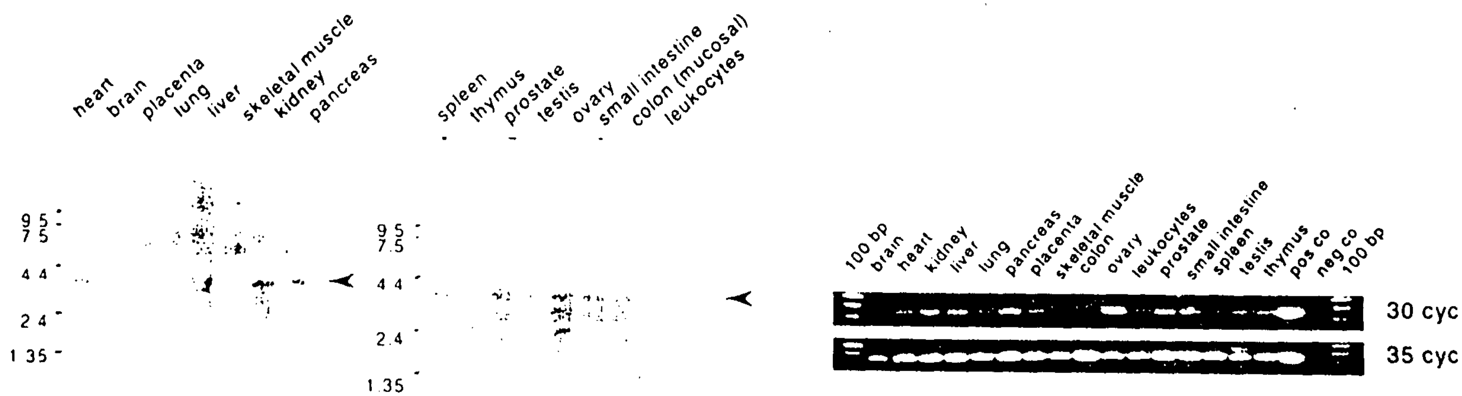

FIG. 29 (CONTINUED). (B)- Tumour tissue and cell lines

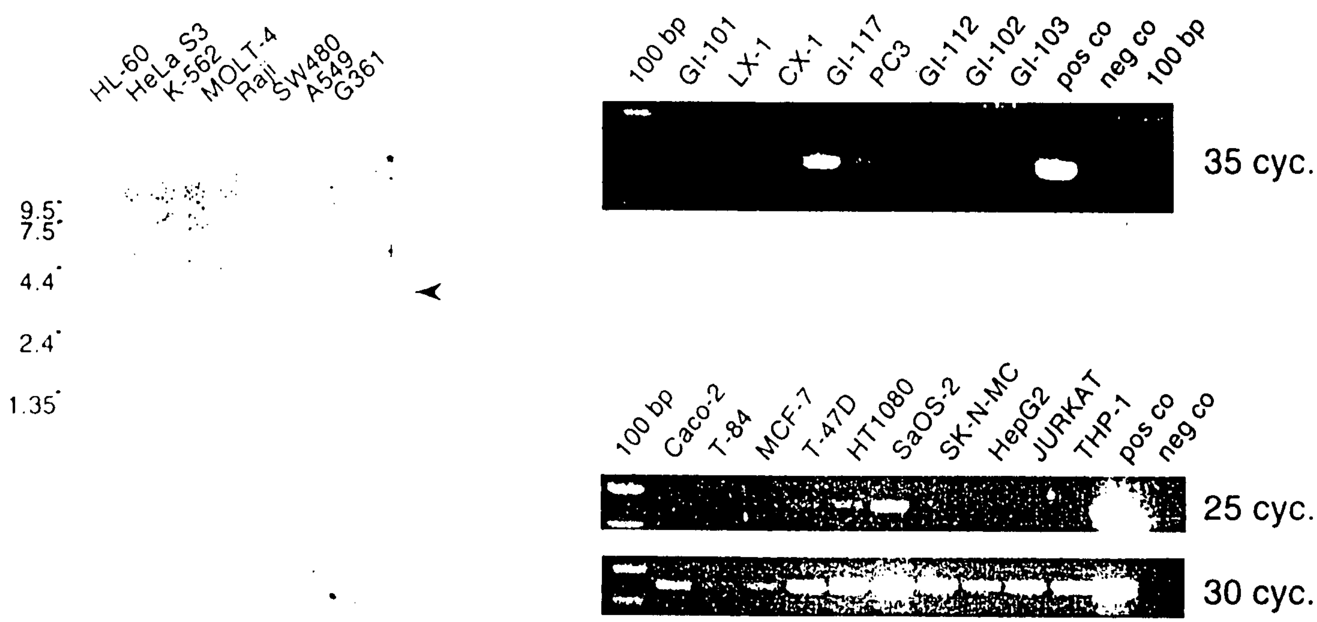

FIG. 30.

Partial intron/exon structure of the VEGF-X gene

(A) - Genomic DNA sequences of 2 exons determined by sequencing

tttcttttataccatatagtggtggatctgaaccagGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCACAGAAGCTGTG
AGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGGAAGACCTTAT
TCGATATCTTGAACCAGAGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTT
TTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTG
TCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCCTG
TTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGgtaggtatacaatttcttttt
ggtttccttcgggtattttatgtctt

aaagccagtcatagacattcgttgatttttaaaagtggcttactcttattccctttcagGTCCTTCAGTTGAGACCAAAGACCGGT
GTCAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGG
ATAGCCGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCAT
CCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAG
GAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTATT
AAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAG
GGTAATGTCAGTACAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGGCTTAACTCTAAAGCTCCATGTCCTGGGC
CTAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTGCGCATATTCACATATGTAAACCAGAACATTCTATGTACTACAAACC
TGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAAACTTGTGTCATGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAA
AATTTCTGCCATTTAGAAGAAGAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTA
TCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTA
AATATATCTATTTTTACCAAAGGTATTTAATATTCTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAAATTTTTCTAA
ACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCATTCTCGTATGGTG
CTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAAGACTTTTTGAAAATAATTAAATTA
TCATATCTTCCATTCCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGAAAGTAGACATTCAGATCCAGCCATTACTAACCTAT
TCCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGCACCTTGAAAAAGACTTGGCAGCTTCCTGATAAAGCGTGCTG
TGCTGTGCAGTAGGAACACATCCTATTTATTGTGATGTTGTGGTTTTATTATCTTAAACTCTGTTCCATACACTTGTATAAATACA
TGGATATTTTTATGTACAGAAGTATGTCTCTTAACCAGTTCACTTATTGTACTCTGGCAATTTAAAAGAAAATCAGTAAAATATTT
TGCTTGTAAAATGCTTAATATCGTGCCTAGGTTATGTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAAATAAAAGAATGT
GGCTATTTTGGGGAGAAAATTatgtgtgtgtgctcaagatttatttcttggactctgagaaatgaaagataaa

FIG. 30 (CONTINUED 1). 48/54

(B) - Location of splice sites within the cDNA sequence

1 GAATTCGCCC TTTTGTTTAA ACCTTGGGAA CTGGTTCAGG TCCAGGTTTT GCTTTGATCC

61 TTTTCAAAAA CTGGAGACAC AGAAGAGGGC TCTAGGAAAA AGTTTTGGAT GGGATTATGT

121 GGAAACTACC CTGCGATTCT CTGCTGCCAG AGCAGGCTCG GCGCTTCCAC CCCAGTGCAG

181 CCTTCCCCTG GCGGTGGTGA AAGAGACTCG GGAGTCGCTG CTTCCAAAGT GCCCGCCGTG

+3 M S L F G L L L L T S
241 AGTGAGCTCT CACCCCAGTC AGCCAAATGA GCCTCTTCGG GCTTCTCCTG CTGACATCTG

+3 A L A G Q R Q G T Q A E S N L S S K F Q
301 CCCTGGCCGG CCAGAGACAG GGGACTCAGG CGGAATCCAA CCTGAGTAGT AAATTCCAGT

+3 F S S N K E Q N G V Q D P Q H E R I I T
361 TTTCCAGCAA CAAGGAACAG AACGGAGTAC AAGATCCTCA GCATGAGAGA ATTATTACTG

+3 V S T N G S I H S P R F P H T Y P R N T
421 TGTCTACTAA TGGAAGTATT CACAGCCCAA GGTTTCCTCA TACTTATCCA AGAAATACGG

+3 V L V W R L V A V E E N V W I Q L T F D
481 TCTTGGTATG GAGATTAGTA GCAGTAGAGG AAAATGTATG GATACAACTT ACGTTTGATG

+3 E R F G L E D P E D D I C K Y D F V E V
541 AAAGATTTGG GCTTGAAGAC CCAGAAGATG ACATATGCAA GTATGATTTT GTAGAAGTTG

+3 E E P S D G T I L G R W C G S G T V P G
601 AGGAACCCAG TGATGGAACT ATATTAGGGC GCTGGTGTGG TTCTGGTACT GTACCAGGAA

+3 K Q I S K G N Q I R I R F V S D E Y F P
661 AACAGATTTC TAAAGGAAAT CAAATTAGGA TAAGATTTGT ATCTGATGAA TATTTTCCTT

+3 S E P | G F C I H Y N I V M P Q F T E A V
721 CTGAACCAG|G GTTCTGCATC CACTACAACA TTGTCATGCC ACAATTCACA GAAGCTGTGA

+3 S P S V L P P S A L P L D L L N N A I T
781 GTCCTTCAGT GCTACCCCCT TCAGCTTTGC CACTGGACCT GCTTAATAAT GCTATAACTG

+3 A F S T L E D L I R Y L E P E R W Q L D
841 CCTTTAGTAC CTTGGAAGAC CTTATTCGAT ATCTTGAACC AGAGAGATGG CAGTTGGACT

+3 L E D L Y R P T W Q L L G K A F V F G R
901 TAGAAGATCT ATATAGGCCA ACTTGGCAAC TTCTTGGCAA GGCTTTTGTT TTTGGAAGAA

+3 K S R V V D L N L L T E E V R L Y S C T
961 AATCCAGAGT GGTGGATCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC AGCTGCACAC

+3 P R N F S V S I R E E L K R T D T I F W
1021 CTCGTAACTT CTCAGTGTCC ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTTCTGGC

+3 P G C L L V K R C G G N C A C C L H N C
1081 CAGGTTGTCT CCTGGTTAAA CGCTGTGGTG GGAACTGTGC CTGTTGTCTC CACAATTGCA

+3 N E C Q C V P S K V T K K Y H E | V L Q L

FIG. 30 (CONTINUED 2).

+3 R P K T G V R G L H K S L T D V A L E H
1201 GACCAAAGAC CGGTGTCAGG GGATTGCACA AATCACTCAC CGACGTGGCC CTGGAGCACC

+3 H E E C D C V C R G S T G G
1261 ATGAGGAGTG TGACTGTGTG TGCAGAGGGA GCACAGGAGG ATAGCCGCAT CACCACCAGC

1321 AGCTCTTGCC CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAACG TATGCGTTAT

1381 CTCCATCCTT AATCTCAGTT GTTTGCTTCA AGGACCTTTC ATCTTCAGGA TTTACAGTGC

1441 ATTCTGAAAG AGGAGACATC AAACAGAATT AGGAGTTGTG CAACAGCTCT TTTGAGAGGA

1501 GGCCTAAAGG ACAGGAGAAA AGGTCTTCAA TCGTGGAAAG AAAATTAAAT GTTGTATTAA

1561 ATAGATCACC AGCTAGTTTC AGAGTTACCA TGTACGTATT CCACTAGCTG GGTTCTGTAT

1621 TTCAGTTCTT TCGATACGGC TTAGGGTAAT GTCAGTACAG GAAAAAAACT GTGCAAGTGA

1681 GCACCTGATT CCGTTGCCTT GCTTAACTCT AAAGCTCCAT GTCCTGGGCC TAAAATCGTA

1741 TAAAATCTGG ATTTTTTTTT TTTTTTTTTG CTCATATTCA CATATGTAAA CCAGAACATT

1801 CTATGTACTA CAAACCTGGT TTTTAAAAAG GAACTATGTT GCTATGAATT AAACTTGTGT

1861 CATGCTGATA GGACAGACTG GATTTTTCAT ATTTCTTATT AAAATTTCTG CCATTTAGAA

1921 GAAGAGAACT ACATTCATGG TTTGGAAGAG ATAAACCTGA AAAGAAGAGT GGCCTTATCT

1981 TCACTTTATC GATAAGTCAG TTTATTTGTT TCATTGTGTA CATTTTTATA TTCTCCTTTT

2041 GACATTATAA CTGTTGGCTT TTCTAATCTT GTTAAATATA TCTATTTTTA CCAAAGGTAT

2101 TTAATATTCT TTTTTATGAC AACTTAGATC AACTATTTTT AGCTTGGTAA ATTTTTCTAA

2161 ACACAATTGT TATAGCCAGA GGAACAAAGA TGATATAAAA TATTGTTGCT CTGACAAAAA

2221 TACATGTATT TCATTCTCGT ATGGTGCTAG AGTTAGATTA ATCTGCATTT TAAAAAACTG

2281 AATTGGAATA GAATTGGTAA GTTGCAAAGA CTTTTTGAAA ATAATTAAAT TATCATATCT

2341 TCCATTCCTG TTATTGGAGA TGAAAATAAA AAGCAACTTA TGAAAGTAGA CATTCAGATC

2401 CAGCCATTAC TAACCTATTC CTTTTTTGGG GAAATCTGAG CCTAGCTCAG AAAAACATAA

2461 AGCACCTTGA AAAGACTTG GCAGCTTCCT GATAAAGCGT GCTGTGCTGT GCAGTAGGAA

2521 CACATCCTAT TTATTGTGAT GTTGTGGTTT TATTATCTTA AACTCTGTTC CATACACTTG

2581 TATAAATACA TGGATATTTT TATGTACAGA AGTATGTCTC TTAACCAGTT CACTTATTGT

2641 ACCTGGAAGG GCGAATTCTG CAGATATC

FIG. 31.

The Effect of FL-VEGF-X on HUVEC Proliferation:
(24-hour serum starvation followed by
one day-treatment)

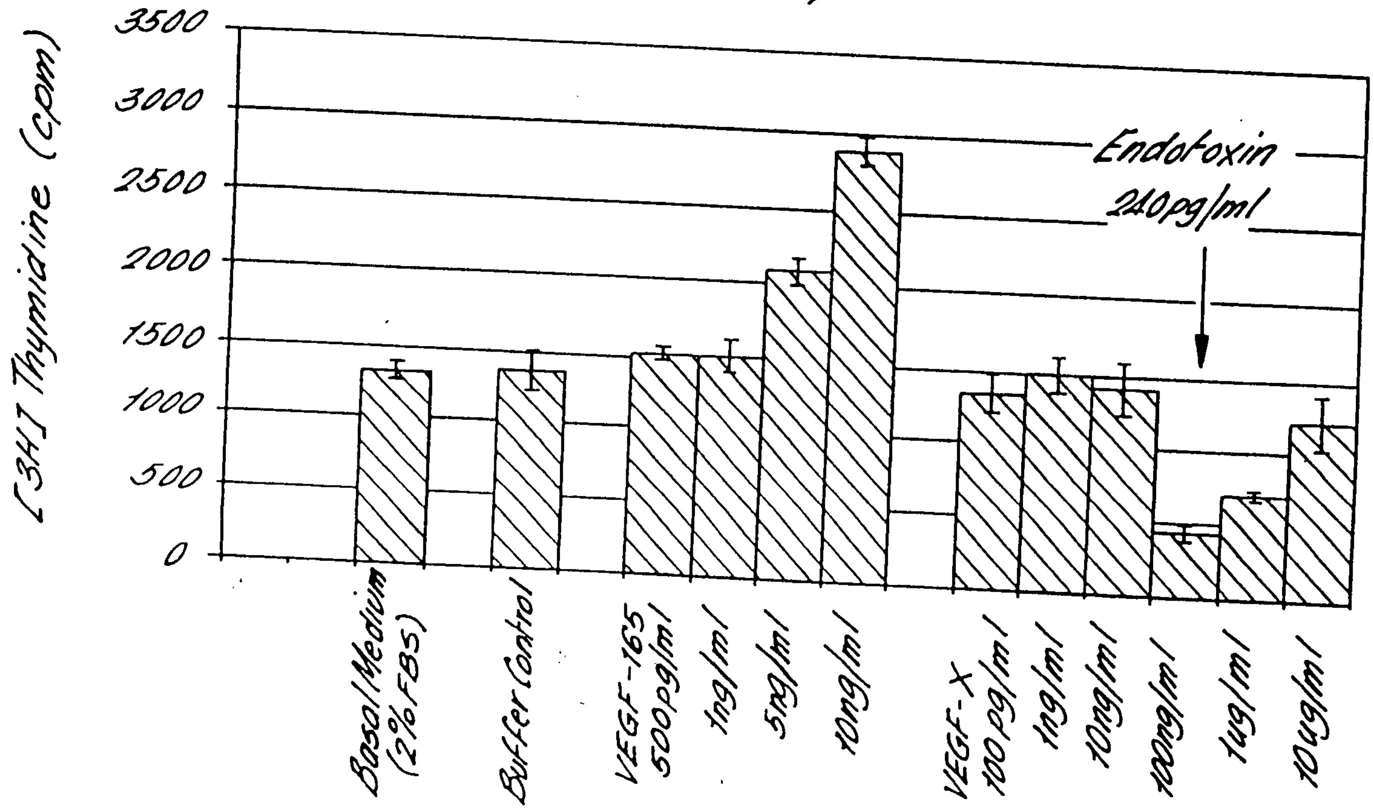

FIG. 32.

The Combined Effect of Truncated VEGF-X (CUB domain) and Human Recombinant $VEGF_{165}$ on HUVEC Proliferation: (24-hour serum starvation followed by two-day-treatment)

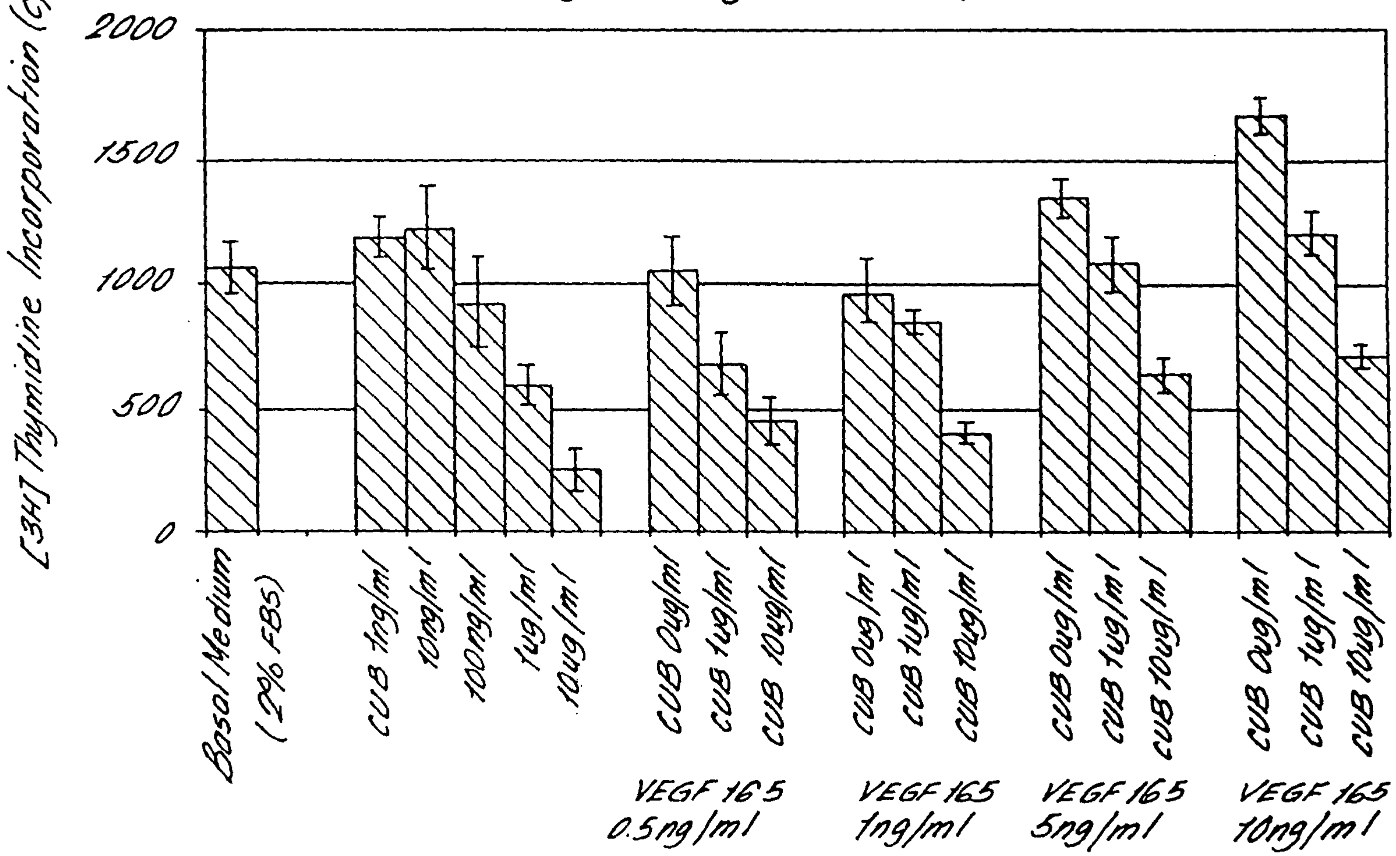

FIG. 33.

The Combined Effect of CUB Domain and Human Recombinant bFGF on HUVEC Proliferation: (24-hour serum starvation followed by two-day-treatment).

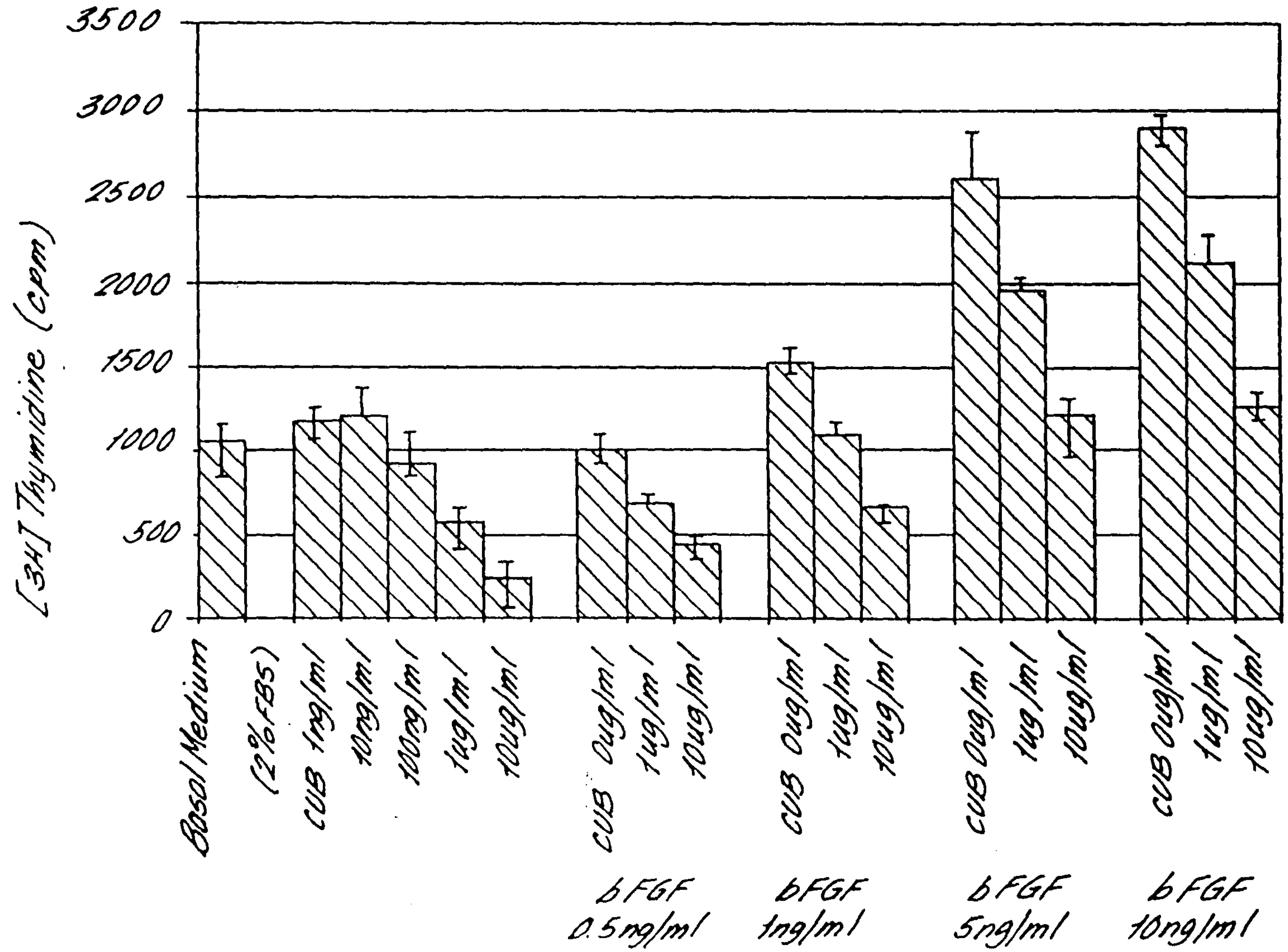

FIG. 34.

LDH Assay for Testing Cytotoxicity of CUB Domain or CUB Domain with rh $VEGF_{165}$

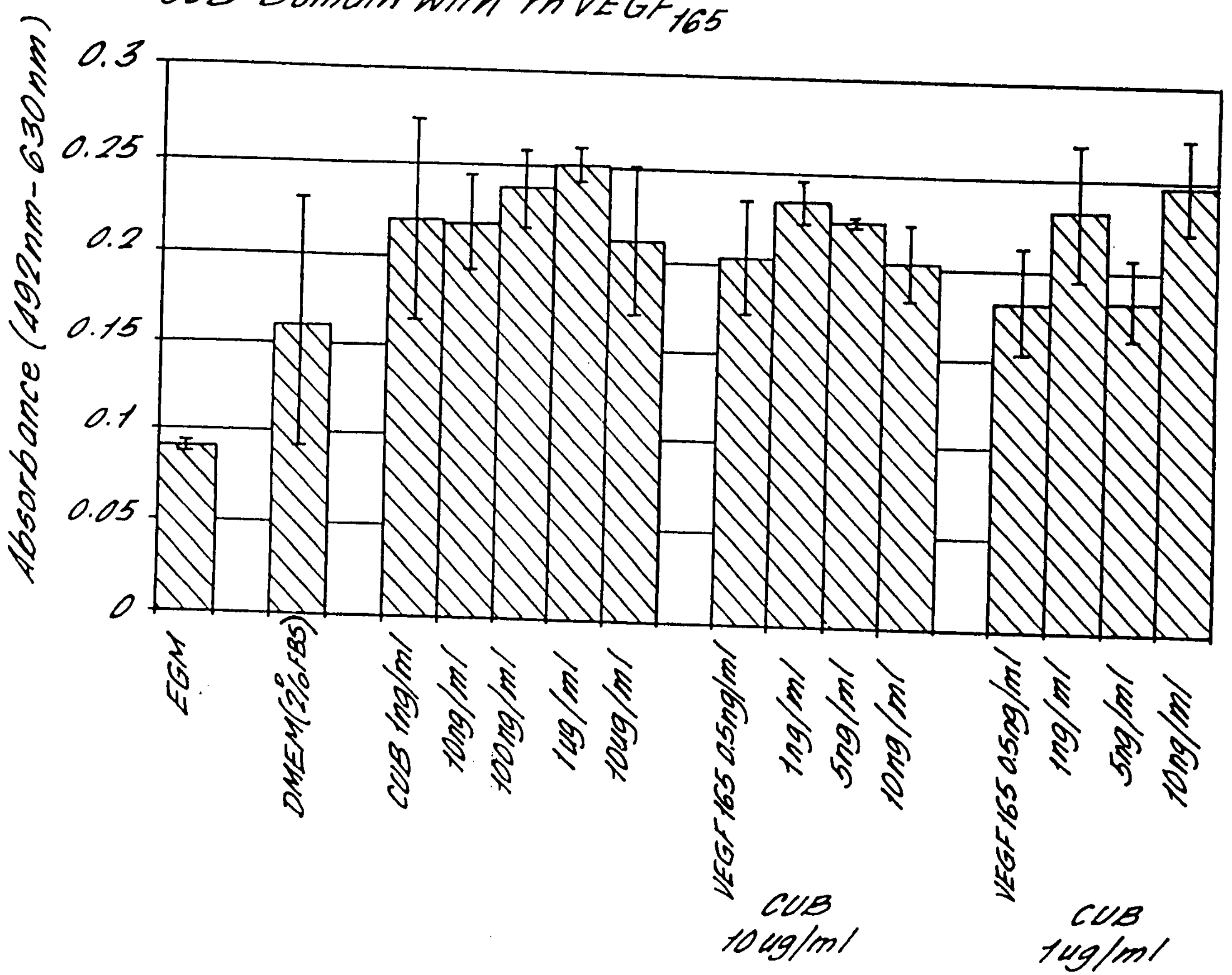

FIG. 35.

LDH Assay for Testing Cytotoxicity of CUB Domain or CUB Domain with rh-bFGF